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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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December 8, 2002, 15:56:19; Search time 15.2491 Seconds (without alignments) 5249.015 Million cell updates/sec
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Copyright (c) 1993 - 2002 Compugen Ltd.
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-995-659-12
US-09-215-649A-12
US-09-577-780-12
US-09-577-780-13
US-08-995-659-10
US-08-995-659-10
US-08-995-659-10
US-08-995-659-10
US-08-98-362-1
US-08-98-362-1
US-09-03-574-22
US-09-03-574-22
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US-09-03-574-21
US-09-03-574-3
US-09-03-574-3
US-09-03-574-3
       US-09-003-574-30
                             US-09-003-574-32
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Sequence 22, Appli
Sequence 22, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 21, Appli
Sequence 21, Appli
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Sequence 1, Appli
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               Sequence 30,
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US-08-996-139-12
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patent No. 6017729
GENERAL INFORMATION:
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APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

COMPUTER: Apple Power Macintosh

COPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:
                                                           TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/1
EILING DATE: 14 OCTOBER 1997
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
USSN 0
APPLICATION NUMBER: USSN 0
APPLICATION NUMBER: 07 MARCH 1997
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                                                                                                                                                                                                         FILING DATE: 07 MARC PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 51 Uncertainty: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                        FILING DATE:
HYPOTHETICAL:
             MOLECULE TYPE:
                                                                                                                                NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851
                           TOPOLOGY:
                                     STRANDEDNESS:
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US-09-003-574-2
US-09-003-570-2
US-09-003-570-2
US-09-003-570-2
US-09-003-570-29
US-07-824-447-47
US-08-469-203A-7
US-08-469-203A-7
US-08-469-203A-7
US-08-469-203A-7
US-08-469-203A-7
US-08-926-522-12
US-09-003-570-21
US-09-003-570-21
US-08-463-262A-1
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Sequence 2, Appli
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Sequence 29, Appl
Sequence 29, Appli
Sequence 47, Appli
Sequence 47, Appli
Sequence 7, Appli
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47, Appl
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ANTI-SENSE: NO ORIGINAL SOURCE:

ORGANISM:

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RESULT 2
US-08-995-659-12
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Patent No. 624222
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Patent No. 624222
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  CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
USSN 08/772,330
                                            CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILLING DATE: 14 OCTOBER 1997
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-996-139-12
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 181;
                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                         STREET:
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CLONE: huRANKL (full length)
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LOCATION: 1..
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74.8%; Pred. No. 1.3e-34;
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RESULT 3
US-09-215-649A-12
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; LOCATION:
US-08-995-659-12
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Best Local Similarity
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
                                                                                                                                                                                                                                                                                                                                                         713 TA 714
                                                                                                                                                                                                                                                                                                                                                                                  653 CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGGTACAGAGTATCTTCAAC 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             533 GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTTGGGCCCAAGATCTCCA 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473 GCÁAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCÁTCTG 532
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HYPOTHETICAL: NATI-SENSE: NO
                                                                                                                                                                       APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Bugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: HOMO IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins Datain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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STRANDEDNESS: single
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REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE FOOR NUMBER: 34,693
                                                                                          COUNTRY: USA
                                                                                                           ADDRESSEE: Immunex Corporation STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           huRANKL (full length)
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                                                                                                                                 Immunex Corporation, Law Department
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SOFTWARE: Microsoft Word for Power Macintosh 6.0.1 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

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SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-215-649A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: 1996
APPLICATION NUMBER: 1996
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                               Sequence 12, Application US/09577780 Patent No. 6419929
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 2851-A REFERENCE/DOCKET NUMBER: 2851-A TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430 TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                             533 GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTTGGGCCAAGATCTCCA 592
                                                                                                                                                                                                              593 ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG 652
                                                                                                                                                                                                                                                                                                  122 ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        64 GCT--CATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                 4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTAATTACCATCAATATCCCATGAG 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
Galibert, Laurent
Maraskovsky, Eugene
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                       APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE: huRANKL (full length)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 121.2; DB 4; Length 954; Pred. No. 1.3e-34;
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US-09-577-780-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: USSN 08/813,509
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: 1996
FILLING DATE: 23 DECEMBER 1996
FILLING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 2852-A
REFERENCE/DOCKET NUMBER: 2852-A
REFERENCE/DOCKET NUMBER: 2852-A
REFERENCE/DOCKET NUMBER: 18952-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 OPERATING SYSTEM: Apple Operating System 7.5.5 OPERATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                       533 GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTTGGGCCAAGATCTCCA 592
                                                                                                   593 ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG 652
                                                                                                                                  122 ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                               176 CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC 235
                                                                                                                                                                                                       64 GCT--CATAAAACGAGTCTTTCTTCGTAAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
236 TA 237
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                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/577,780 FILING DATE: 24-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 954 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE: huRANKL (full length)
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                           46.4%; Score 121.2; DB 4; Length 954; 74.8%; Pred. No. 1.3e-34;
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FILE REFERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052,521C
PRIOR APPLICATION NUMBER: US/09/052,521C
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR FILING DATE: 1997-06-23
PRIOR FILING DATE: 1997-04-16
PRIOR FILING DATE: 1997-04-16
SCOTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (185)..(1135)
US-09-052-521C-3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                         APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                               COUNTRY: UZIP: 98101
                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                            897 TA 898
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                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                      837 CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC 896
                                                                                                                                                                                                                                                                                                                                                                                                          176 CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                777 ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            717 GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTCCA 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
                                                                                                         Seattle
                                                                                            WA
                                                                                                           51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 46.4%; Score 121.2; DB 4; Length 2271; Similarity 74.8%; Pred. No. 2.1e-34; 81; Conservative 0; Mismatches 53; Indels 8;
                                                                            USA
                                                                                                                Immunex Corporation, Law Department
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Sequence 10, Application US/08995659
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                                                                                 645 CT 646
                                                                                                       585 GCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG 644
                                                                                                                        175 GCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAG 234
                                                                                                                                                           525 AACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC 584
                                                                                                                                                                           121 AACATGAGTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAAT 174
                                                                                                                                                                                                              465 GGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCT 524
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TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                               405 GGCAAGCCTGAGGCCAGCCATTTGCACACCACCATCAATGCTGCCAGCATCCCATCG 464
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HYPOTHETICAL: NC
                                                                                                                                                                                                                               63 GG--CTCATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
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                                                                                                                                                                                                                                                                                 3 GGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGA 62
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 07 MARCI PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
USSN 60/064,671
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CLASSIFICATION: DECEMBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lir
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PTI.TNG DATE: 23 DECEMBER 1996
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                                                                                                                                                                                                                                                                                                                       36.6%; Score 95.6; DB 3; Length 1630; 68.2%; Pred. No. 4.2e-25; ative 0; Mismatches 69; Indels 8
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GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M. APPLICANT: Galibert, Laurent

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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
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OPERATING SYSTEM: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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PRIOR APPLICATION DATA:
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CLASSIFICATION:
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CLASSIFICATION:
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HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: RANKL
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                                                                                                                                                                                                                      405 GGCAAGCCTGAGGCCCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCG 464
                           121 AACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAAT 174
                                                                                                           465 GGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 3..884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY:
525 AACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC 584
                                                                                                                                      63 GG--CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
                                                                                                                                                                                                                                                                             3 GGCAATCCTGAGGCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGA 62
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                                                                                                                                                                                                                                                                                                                                                            Similarity 68.2%; Pred. No. 4.2e-25; Similarity 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunex Corporation, Law Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: US/08/995,659
22 DECEMBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 OCTOBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USSN 60/064,671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USSN 08/813,509
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                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 69; Indels 8; Gaps
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RESULT 8
US-09-215-649A-10
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Patent NO. 6271349
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   585 GCCAACATTTGCTTTCGGCATCATGAAACATCGGGGAAGCGTACCTACAGACTATCTTCAG 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 GCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAG 234
                                                             US-09-215-649A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         645 CT 646
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Best Local Sir
Matches 165;
                            Query Match
                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
NAME: Perkins, UMBER: 34,693
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEPAX: (206)233-0644
TELEPAX: (206)233-0644
                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
                                                                                NAME/KEY: CDS
IOCATION: 3..884
IOCATION: SEQ ID NO: 10:
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                           ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/996,139
ETLING DATE: <UNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION DATE: 23 DECEMBER 1996
ETLING DATE: 23 DECEMBER 1996
                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 2851-A
                   h 36.6%; Score 95.6; DB 4; Length 1630; Similarity 68.2%; Pred. No. 4.2e-25;
                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                               ORGANISM: Mus musculus
                                                                                                                                               CLONE: RANKL
                                                                                                                                                                 LIBRARY: <Unknown>
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       Conservative
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               0; Mismatches
                                 8; Gaps
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RESULT 9
US-09-577-780-10
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GENERAL INFORMATION:
                                                                                                                                                                                                                                           HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                               NAMÉ: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                585 GCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         465 GETTCCCATANAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GG--CTCATAAAACGAGTCTTTCTTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Anderson, Dirk M.
Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTAATAATACCATCAATATCCCATGA 62
                                                                                                                  LENGTH: 1630 base pairs
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/577,780 FILING DATE: 24-May-2000 CLASSIFICATION: CLASSIFICATION: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09577780
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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LENGTH: 2191 has?
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US-08-989-362-1
                                                                                                                   FILING DAIL.

CLASSIFICATION: 56

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/032,846

APPLICATION NUMBER: 1960/032,846
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Patent No. 6242586
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                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PG-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-577-780-10 DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                            NAME: Ching, Edwin EREGISTRATION NUMBER:
                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gorman, Daniel M. APPLICANT: Mattson, Jeanine D. TITLE OF INVENTION: Mammalian (TITLE OF INVENTION: Reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                           APPLICATION NUMBER: US/0
FILING DATE: 12-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                             STREET: 901 Call
                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   645 CT 646
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                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 GCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               525 AACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465 GETTECCATAAAGTCACTETGTECTETTGGTACCACGATCGAGGCTGGGCCAAGATETCT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405 GGCAAGCCTGAGGCCCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 GG--CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
nucleic acid
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                                                                                                                                                                                                                                                                                                                          94304-1104
      2191 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                   California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165; Conservative
                                                                                                                                                                                                                                                                                                                                                                         901 California Avenue
                                                                                                                                                                                                                                                                                                                                             USA
                                                                (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 3..884
                                                                                                                                                                                                                                                                                                                                                                                    DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: <Unknown>
CLONE: RANKL
                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalian Cell Surface Antigens; Related
                                                                                                          34,090
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                                                                                            DX0686
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US-08-989-362-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                       US-08-842-842-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08842842 Patent No. 5843678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      593 GGCAAGCCTGAGGCCCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCG 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BOYLE, WILLIAM J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          653 GGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCT 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               773 GCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 GCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        833.CT 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 CT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 36.6%;
Local Similarity 68.2%;
es 165; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCCATGA 62
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                        FEATURE:
                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1840 Dehavi:
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GG--CTCATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
                                                                                                      TOPOLOGY:
                                                                                                                     STRANDEDNESS: single
                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                       91230-1789
                                                                                                                                    nucleic acid
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1840 Dehavilland Drive
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                                                                                                                                                   2295 base pairs
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                                                                                                        linear
                                           158..1105
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36.6%; Score 95.6;
                                                                                                                                                                                                                                                                               US/08/842,842
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     DB 2;
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     Length 2295;
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Query Match

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866 CT 867

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US-09-052-521C-1
                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (158)..(1105)
US-09-052-521C-1
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Boyle, William J. TITLE OF INVENTION: Osteopro
                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/1
PRIOR FILING DATE: 1997-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2295
TYPE: DNA
ORGANISM: Mouse
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                626 GGCAAGCCTGAGGCCCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCG 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            686 GGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCT 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 746 AACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAAT 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 GG--CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGA 62
                                                                                                                                                                                                                                              626 GGCAAGCCTGAGGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCG 685
                                                                                                                                                                         686 GGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCT 745
                                     806 GCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG 865
                                                                     175 GCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAG 234
                                                                                                         746 AACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC 805
                                                                                                                                       121 AACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAAT 174
     235 CT 236
                                                                                                                                                                                               63 GG--CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
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es 165; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.2%; Pred. No. 5.1e-25; tive 0; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Osteoprotegerin Binding Proteins and Receptors
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RESULT 13

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US-09-003-570-22
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                                                                                                                                                                                                                       Patent No. 6281345
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                      Matches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                        APPLICANT: Tripp, Cynthia Ann
APPLICANT: Frank, Glenn R.
APPLICANT: Grieve, Robert B.
TITLE OF INVENTION: MCTALLOENDOPEPTIDASE GE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (303) 863-02:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 271 base pairs
                                                                       ADDRESSEE: SHERIDAN NOO: .... SUITE 3500
                                                  COUNTRY:
                                                                    STATE:
                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOTTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: SHERIDAN ROSS P.C.
STREET: 1700 LINCOLN ST., SUITE 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tripp, Cynthia Ann
APPLICANT: Frank, Glenn R.
APPLICANT: Grieve, Robert B.
TITLE OF INVENTION: NOVEL PARASITE ASTACIN
TITLE OF INVENTION: METALLOENDOPEPTIDASE PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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STATE:
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CITY: DENVER
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                                                                                                                                   METALLOENDOPEPTIDASE GENES
                                                                                                                                                                                                                                                                                                                                                                                11.4%; Score 29.8; DB 4; Length 271; 70.2%; Pred. No. 0.2;
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US-09-003-574-20
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Patent No. 6265198
GENERAL INFORMATION:
                                                                                        TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                  REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 863-9700
MOLECULE TYPE:
                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Grieve, Robert B.
TITLE OF INVENTION: NOVEL PARASITE ASTACIN
TITLE OF INVENTION: METALLOENDOPEPTIDASE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tripp, Cynthia Ann
APPLICANT: Frank, Glenn R.
APPLICANT: Grieve, Robert B
                        TYPE: nucleic acid
STRANDEDNESS: single
               TOPOLOGY:
                                                          LENGTH:
                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/003,574
                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                         FILING DATE:
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CURRENT APPLICATION DATA:
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1700 LINCOLN ST., SUITE 3500
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OM nucleic - nucleic search, using sw model
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Perfect score:
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Maximum DB seq length: 200000000
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1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
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Copyright (c) 1993 - 2002 Compugen Ltd.
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               /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
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      100%
                           US-08-996-139-12
US-08-995-639-12
US-09-215-649A-12
US-09-577-780-12
US-09-577-780-13
US-08-995-639-10
US-08-995-639-10
US-08-995-639-10
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US-08-98-362-1
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US-09-215-649A-10
US-09-244-796-17
US-09-244-796-17
US-09-258-102-1
US-09-568-102-1
US-09-568-102-1
US-09-568-486-1
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                                                                                                                                                               Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 10, Appl
Sequence 1, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 14, Appli
Sequence 14, Appli
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Patent No. 6017729
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                    COMPUTER TEADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

SOFTWARE: MICROSOFT NOT NOT 120

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                  TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                     APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                        FILING DATE: 07 MARC PRIOR APPLICATION DATA:
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32.8
32.8
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                                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                          MOLECULE TYPE:
                               HYPOTHETICAL:
                                                                                                                                                                                                                                       APPLICATION NUMBER: USSN OF FILING DATE: 07 MARCH 1997
                                                                                                                                                      NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 285
                                                                                                                                    TELEPHONE:
                                                       TOPOLOGY:
                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                  WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galibert, Laurent
Maraskovsky, Eugene
                                                                            nucleic acid
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                                                        linear
                                                                                                                                     (206)587-0430
                                                                                                                                                                                                                                                                                                                      22 DECEMBER 1997
                                               CDNA
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                                                                   single
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US-08-59-252-103
PCT-US96-06352-103
PCT-US96-06353-103
US-08-868-577-18
US-09-688-577-18
US-09-262-749-1
US-09-262-749-1
US-09-603-567-1
US-09-603-567-1
US-09-603-567-1
US-09-603-567-1
US-09-603-567-1
US-09-603-567-245
US-09-902-451-245
US-09-902-451-245
US-09-062-451-245
US-09-062-451-245
US-09-07-005-32
US-09-07-005-32
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sequence 10, Appl
sequence 18, Appl
sequence 1, Appli
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sequence 1, Appli
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Sequence 103, App
Sequence 103, App
Sequence 103, App
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ANTI-SENSE: ORIGINAL SOU

SOURCE:

IMMEDIATE SOURCE:

Homo sapiens

LIBRARY: ORGANISM:

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US-08-995-659-12
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Patent No. 6242213
GEMERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
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                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07 MARCH
                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
                                                                                                                                                                                     ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.
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US-08-996-139-12 1..951
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APPLICANT: Galibert, Laurent
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                       STREET: Seattle
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                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 98101
                                                                                                            CLASSIFICATION
                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 22 DEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                          22 DECEMBER 1997
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                                                                     USSN 08/813,509
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RESULT 3
US-09-215-649A-12
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LOCATION: 1...
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COMPUTER: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
                                                                                                                                                                                                                                                                                                                                                       629 AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG 688
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SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                           569 ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC 628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                   TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                  APPLICANT: Anderson, Dirk M. Galibert, Laurent Maraskovsky, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
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HYPOTHETICAL:
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Local Similarity 72.6%;
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TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193;
                                                                                   COUNTRY: USA
                                                                                                 CITY: Seattle
STATE: WA
                                                                                                          ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
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US-09-215-649A-12
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                                                                                Sequence 12, Application US/09577780 Patent No. 6419929
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO: 12:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 583 ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA--- 639
                                                                                                                                                                                                                                                                                                                                          629 AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG 688
                                                                                                                                                                                                                                                     689 ACCTAGCTACAGAGTATCTTCAACTA 714
                                                                                                                                                                                                                                                                                                 697 GCCTAACTCTGCAGGACCTTCAGCTA 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: cDNA
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
                                            APPLICANT: Anderson, Dirk M.
Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC 628
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FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 28
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TYPE: nucleic acid
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LOCATION: 1..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE: huRANKL (full length)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206)587-0430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: <Unknown>
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72.6%;
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US-09-577-780-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/995,659
ETLING DATE: «Unknown»
APPLICATION NUMBER: USSN 08/813,509
ETLING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                          465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                                                                                                                                               449 CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 508
           697 GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                           629 AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG 688
                                                                                                    640 ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                                                                   569 ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC 628
                                                                                                                                                                                            583 ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA--- 639
                                                                                                                                                                                                                                       509 TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG 568
                                                                                                                                                                                                                                                                                    525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98101
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/577,780 FILING DATE: 24-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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Patent No. 6017729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 08/0 PRIOR FILING DATE: 1997-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteopro
FILE REFERENCE: A-451Brv
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SOFTWARE: Patentin Ver.
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                 COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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NAME/KEY: CDS
LOCATION: (185)..(1135)
                                                                                                                                                                                                                      APPLICANT: Anderson, Dirk M. APPLICANT: Galibert, Laurent APPLICANT: Maraskovsky, Eugene
                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                   TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                              873 ACCTAGCTACAGAGTATCTTCAACTA 898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              813 AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       583 ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA--- 639
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COMPUTER: Apple Power Macintosh
                                                                                                   STATE:
                                                                                                                                    STREET:
                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 10.9%;
Local Similarity 72.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193; Conservative
                                                                                                               Seattle
                                                                                                 WA
                                                                                                                                E: Immunex Corporation, Law Department
1 University Street
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RESULT 7
US-08-995-659-10
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: RANKL FEATURE:
                                                                                                                                   574 ATTACCTGTACGCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus
IMMEDIATE SOURCE:
                                                                      634 ACTATCTTCAGCT 646
                                                                                                        709 AGGACCTTCAGCT 721
                                                                                                                                                                                                         514 CCAAGATCTCTAACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCT 573
                                                                                                                                                                                                                                           595 CAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTT 648
                                                                                                                                                                                                                                                                             454 GCATCCCATCGGGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGG 513
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LENGTH: 1630 base pairs
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: USSN
FILING DATE: 23 DECEMBER
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                    537 ATATCCCATGAGG--CTCATAAAACGAGTCTTTCTTCTTGGAAAGATGACCAAGATTGGG 594
                                                                                                                                                                                                                                                                                                                                                  394 TGGCCCAGCGAGGCAAGCCTGAGGCCAGCCATTTGCACACCTCACCATCAATGCTGCCA 453
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APPLICATION NUMBER:
FILING DATE: 07 MARC
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SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
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Sequence 10, Application Patent No. 6242213
GENERAL INFORMATION:
APPLICANT: Anderso

Application US/08995659

APPLICANT:

Anderson, Dirk M. Galibert, Laurent

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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US
PILING DATE: O7 MARCH
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: PERKINS, PATRICIA Anne REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 2852 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pair
                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 51 Seattle
     514
                595 CAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTT 648
                                                                                        537 ATATCCCATGAGG--CTCATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGG
                                                                                                                                                                      477 TTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCA 536
                                                                                                                                    394 TGGCCCAGCGAGGCAAGCCTGAGGCCCAGCCATTTGCACCACCTCACCATCAATGCTGCCA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Perkins, Patricia REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 3..884
                                                                                                                                                                                                                                                                                                                                                      CLONE:
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                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: USSN 08/7 FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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CCAAGATCTCTAACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCT 573
                                                                    GCATCCCATCGGGTTCCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1630 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :: (206)587-0430
(206)233-0644
POR SEQ ID NO: 10:
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                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER: USSN 60/064,671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 DECEMBER 1997
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67.2%;
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                                                                                                                                                                                                                           Score 97; DB 4;
Pred. No. 8e-22;
                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                            75;
                                                                                                                                                                                                                                           Length 1630;
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                          8
                                                                                                                                                                                                         Gaps
                                                                                                     594
                                                                   513
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; LOCATION: 3..884; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-215-649A-10
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      Matches 170;
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                             FEATURE
                                                                                                                                                                                                                    ORGANISM: Mus musculus IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGC 708
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                                                                                                                  NAME/KEY: CDS
LOCATION: 3..884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/996,139
FILING DATE: <UNKNOWN>
PAPPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                               LIBRARY: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1630 base pairs
                                                                                                                                                                               ONE: RANKL
      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98101
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                      8.4%;
67.2%;
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    0,
                    Score 97; DB 4; Length 1630; Pred. No. 8e-22;
    Mismatches
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    75;
Gaps
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Indels

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GENERAL INFORMATION:
                                                                                                                                                                                                                                                TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           514 CCAAGATCTCTAACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGCCTTCT 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        595
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APPLICATION NUMBER: 08/995,659

FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patticia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS:
                                                 ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pa
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
IMMEDIATE SOURCE:
                                                                                              HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATATCCCATGAGG--CTCATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGG 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATCCCATCGGGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.
SOFTWARE: Microsoft Word for Power Macintos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/577,780 FILING DATE: 24-May-2000 CLASSIFICATION: <Unknown>
                             ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: WA
COUNTRY: USA
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Maraskovsky, Eugene
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US-08-989-362-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-09-577-780-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1,
                                                                                      APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (550)852-9196
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               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2191 base pair
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                            CLASSIFICATION: 56
PRIOR APPLICATION DATA:
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APPLICANT: Mattson,
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                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08 FILING DATE: 12-DEC-1997
                                                                        TELEFAX:
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Pred. No.
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US-08-842-842-6
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US-08-842-842-6
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Best Local Similarity 67.2%;
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Query Match
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                                                                                                                                                                                       NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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pred. No. 9.7e-22;
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US-09-052-521C-1
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SEQ ID NO 1
LENGTH: 2295
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TITLE OF INVENTION: Osteopro
FILE REFERENCE: A-451Brv
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LOCATION: (158)..(1105)
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                                                                                                     649 ATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGC 708
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855 ACTATCTTCAGCT 867
                                        709 AGGACCTTCAGCT 721
                                                                              795 ATTACCTGTACGCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAG 854
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0; Mismatches 75; Indels
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US-08-232-463-14/c
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                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5670367
GENERAL INFORMATION:
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                             356 CAAGGCACCAGGCATTTTTGAGCATTTGGGATTTGTCAGCAAACAAGTCAGACAAAAAA 415
                                                                                           296 GGGGAGAGAAGTGGAGAGAGGACCTGGAGGGCCAGTAGAAGGTATGCACAAAGTATCTA 355
                                                                                                                                                                                                                     176 CTTCAGGAACACCCTGCTTGAGAGGCCTGTGAGAGGTGGGGAATCAATACCTGACCTCGC 235
                                                                                                                                                                                                                                                                                  116 GGGATAAGGACGTGGTTGCGAGGACATGGAGGGAAAGTTCTACAGAGGAGGCACAGTGGG 175
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                         236 TCTCCTTCCATCTCTCCCCAACCCACAGGGGTTGGTGTGTGGGCCCCACAGGCGAGCCTCCC 295
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CURRENT APPLICATION DATA:
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BENT, Stephen A REGISTRATION NUMBER: :
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GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.

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US-09-244-796-17

; Sequence 17, Application US/09244796

; Patent No. 6281344
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APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6258558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: (1)...(289)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                      1009 TGTAACTCTGAACCACAGGACAAAGCATGATGTGATG 1045
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                                                                                                                181 RSRNRNRSRNRNRSRNRNRSRNRNRSRNRNR 217
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4.6%; Pred. No. 0.021;
vative 98; Mismatches 109; Indels
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APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: SUSIONS
FILE REFERENCE: 007186/350007
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/034,491
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-07
SEARLIER FILING DATE: 1998-01-14
NUMBER OF SEO ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
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: LOCATION: (1)...(289)

: OTHER INFORMATION: n = A,T,C or G

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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation template
FEATURE:
                                                                                                                                                                        1009 TGTAACTCTGAACCACAGGACAAAGCATGATGTGATG 1045
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Maximum Match 100%
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
      US-08-996-139-12
US-08-995-659-12
US-09-215-649A-12
US-09-215-649A-10
US-08-995-659-10
US-08-995-659-10
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US-08-989-362-1
US-08-989-362-1
US-08-989-362-1
US-08-9842-842-6
US-09-052-521C-1
US-08-464-842-6
US-09-052-521C-1
US-08-464-273A-7
US-08-469-203A-7
US-08-469-203A-7
US-08-469-203A-7
US-08-469-203A-7
US-08-68-964-14
US-08-768-964-15
US-09-055-299-15
US-09-055-299-15
US-09-055-299-15
US-08-968-964-11
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                                                                                                                                                                       Sequence 5, Appl
Sequence 47, Appl
Sequence 47, Appl1
Sequence 9, Appl1
Sequence 7, Appl1
Sequence 7, Appl1
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Sequence 12, Appl
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Sequence 10, Appl
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6, Appli
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FILING DATE: 14 OCTOBER 1997 FILING DATE: 10 OCTOBER 1997 RIOR APPLICATION NUMBER: USSN 08/813 FILING DATE: 07 MARCH 1997 FILING DATE: 07 MARCH 1997 FILING DATE: 07 MARCH 1997 FILING DATE: 08 NOBER: 08/772 APPLICATION NUMBER: USSN 08/772 APPLICATION NUMBER: 34.693 FILING DATE: 23 DECEMBER 1996 FILING DATE: 23 DECEMBER: 34.693 REFERENCE/DOCKET NUMBER: 34.693 REFERENCE/DOCKET NUMBER: 2851-2851-2851-2851-2851-2851-2851-2851-	996-139-12 ence 12, Application US/089 ence 12, Application Dirk M pplicaNT: Anderson, Dirk M pplicaNT: Marzskovsky Eug UTILE OF INVENTION: Recepto UMBER OF SEQUENCES: 19 VORRESSPONDENCE ADDRESS: ADDRESSEE: Immunex Corpor STREET: 51 University Str CITY: Seattle STATE: WA COUNTRY: USA ZIP: 98101 ZIP: 98101 ZOMPUTER READABLE FORM: COMPUTER READABLE FORM: APPLICATION NUMBER: USO APPLICATION NUMBER: USO FILING DATE: 22 DECEMBER CLASSIFICATION NUMBER: USSN APPLICATION NUMBER: USSN	28.4 13.9 597 2 US-08-768-964-16 28.4 13.9 597 3 US-09-005-299-11 28.4 13.9 597 3 US-09-005-299-16 28.4 13.9 597 4 US-09-515-431-16 28.4 13.9 597 4 US-09-515-431-16 28.4 13.9 714 2 US-08-768-964-6 28.4 13.9 714 2 US-08-768-964-6 28.4 13.9 714 3 US-09-005-299-6 28.4 13.9 714 3 US-09-05-299-8 28.4 13.9 714 4 US-09-515-431-6 28.4 13.9 714 4 US-09-515-431-6 28.4 13.9 789 2 US-08-768-964-4 28.4 13.9 789 3 US-09-05-299-5 28.4 13.9 789 4 US-09-515-431-4 28.4 13.9 789 4 US-09-515-431-5 28.4 13.9 1069 2 US-08-768-964-1
		Sequence 16, sequence 11. sequence 11. sequence 16. Sequence 16. Sequence 6. Sequence 6. Sequence 6. Sequence 6. Sequence 6. Sequence 7. S
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                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins Patricia
                                                                                                                                                                                                                                                                                 COMMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
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                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
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APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
CORRESPONDENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
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                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
REGISTRATION NUMBER: 34,693
                                                             APPLICATION NUMBER: USSN 08/7 FILING DATE: 23 DECEMBER 1996
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                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                            APPLICATION NUMBER: USSN 60/064,671 FILING DATE: 14 OCTOBER 1997
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 22 DE(
                                                                                                                                                                                                                                                        CLASSIFICATION:
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LOCATION:
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US-09-215-649A-12
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 GCTA 180
   COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
RAPPLICATION DATA:
APPLICATION WIMBER: US/09/215,649A
FILLING DATE: 17-Dec-198
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION UNMBER: 08/996,139
PRIOR APPLICATION UNMBER: 08/996,139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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FILING DATE: <Unknown>
                                                                                                                                                                                                                  ZIP: 98101
                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                  STATE: WA
                                                                                                                                                                                                                                                                  ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                 CITY: Seattle
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US-09-577-780-12
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                                                                                                                                                                                                                                                                    Sequence 12, Application US/09577780 Patent No. 6419929 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     651 TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toca<sub>T</sub>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: HO IMMEDIATE SOURCE:
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                                                                                                                                                                                   Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
                                                                                                                                                                                                                                                       APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137;
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996
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Similarity 74.5%;
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Perkins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE: huRANKL (full length)
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LOCATION: 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: <Unknown>
                                                                                                                                      ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                       STATE: WA
                                                                                                                       CITY: Seattle
                                                                                          COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 96.4; DB 4; Length 954; pred. No. 3.7e-26;
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SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-577-780-12
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                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                     Sequence 3, Application US/09052521C Patent No. 6316408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 12:
EILE REFERENCE: A-451Brv CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30 CURRENT FILING DATE: 1998-08-85 PRIOR APPLICATION NUMBER: 08/880,855 PRIOR FILING DATE: 1997-06-23 PRIOR APPLICATION NUMBER: 08/842,842
                                                                                        APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteopro
FILE REFERENCE: A-451Brv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCCAAGATCTC 590
                                                                                                                                                                                                                                                                                                                                                                                                                                             591 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
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FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft Word for Power Macintosh 6.0.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                           711 ACTA 714
                                                                                                                                                                                                                                                                                                                                177 GCTA 180
                                                                                                                                                                                                                                                                                                                                                                 651 TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO ANTI-CHARTE NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/995,659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 2852-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206)587-04.
TELEFAX: (206)233-0644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: huRANKL (full length)
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LOCATION: 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 954 base pairs
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74.58;
                                                                                                                     Osteoprotegerin Binding Proteins and Receptors
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US-08-996-139-10
APPLICATION UMMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTONNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TÉLECOMMUNICATION INFORMATION:
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SEQ ID NO 3
LENGTH: 2271
TYPE: DNA
ORGANISM: Human
FEATURE:
NAMEXKEY: CDS
LOCATION: (185)...(1135)
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Patent No. 6017729
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                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                            APPLICATION NUMBER: USSN 60/1
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power MacIntosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
ABOUTTO MATTER MICROSOFT MACINTOSH 6.0.1
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                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
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                                                                                                                              APPLICATION NUMBER: USSN 08/813,509 FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/996 FILING DATE: 22 DECEMBER 1997
                                                                                                                                                                                                                                           CLASSIFICATION
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                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 GCTA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             51 University Street
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                                                                                                                                                                                                USSN 60/064,671
                                                                                                                                                                                                                                                                  US/08/996,139
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US-08-995-659-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 125; Conservative
                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 0
FILING DATE: 07 MARCH 1997
                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: USSN 60/064,671
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TELEPAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                 CLASSIFICATION;
                                                                                                APPLICATION NUMBER: FILING DATE: 14 OC'
                                                                                     CLASSIFICATION:
                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 22 DEG
                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  589 ACATTTGGTTTCGGCATCATGAAACATCGGGAAGCGTAGCTACAGACTATCTTCAGCT 646
                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 98101
                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Immunea Conference STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                529 TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 588
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
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LOCATION:
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CLONE: RANKL
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                                                                                                  14 OCTOBER 1997
                                                                                                                                                               22 DECEMBER 1997
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                                          USSN 08/813,509
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                                                                                                                                                                           US/08/995,659
                                                                                                                                                                                                      Word for Power Macintosh 6.0.1
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; LOCATION:
US-08-995-659-10
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 23 DECCLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               529 TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTÁTTACCTGTACGCCA 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469 CCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACA 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: RANKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SENSE:
                                                                                                                                                                                                                                                                                        Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Anderson, Dirk M.
APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                   COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                           ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                            CITY: Seattle
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23 DECEMBER 1996
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                                                                                                                                                                                                                                                                                                                                                  Galibert, Laurent
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                                                                                                                                                                                             USA
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US-09-215-649A-10
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US-09-577-780-10
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                                                                                                                                                                                                                                                                                                                                         , Sequence 10, Application Patent No. 6419929 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          529 TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 CCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO
                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                            Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                    APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/996,139
ETLING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
ETLING DATE: 07 MARCH 1997
ETLING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                    ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                               COUNTRY:
                                                                                                                                                    STATE: WA
                                                                                                                                                                        CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                Application US/09577780
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                                                                                                                   98101
                                                                                                                                   USA
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APPLICATION NUMBER: US/09/577,780 FILING DATE: 24-May-2000

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US-08-989-362-1
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                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08989362
Patent No. 6242586
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
COMPUTER READABLE FORM: 'MEDIUM TYPE: Floppy disk
                                                                                                                                                                       APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
TITLE OF INVENTION: Reagents
                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
                                         COUNTRY: USA
ZIP: 94304-1104
                                                                                                                                                                                                                                                                                                                                                                          589 ACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCT 646
                                                                          CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                              122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                 529 TGACGTTAAGCAAAGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469 CCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACA 528
                                                                                                          ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/995,659
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
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70.2%;
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US-08-842-842-6
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Patent No. 5843678
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: BOYLE, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
                                                                                      OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
REFERENCE/DOCKET NUMBER: A-451
                                                                           FILING DATE:
                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                             COUNTRY: USA
ZIP: 91230-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     777 ACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCT 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 ACATTTGGTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
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                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                      CITY:
                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        657 CCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACA 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CTCATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGGCAAACGTCTCCAACA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 39.6%; Score 80.8; DB 4; Length 2191; Local Similarity 70.2%; Pred. No. 3.7e-20; es 125; Conservative 0; Mismatches 47; Indels 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ching, Edwin P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                            Thousand Oaks
: California
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                                                                                                                                                                                                                                                                           1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2191 base pairs
                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                              Amgen Inc.
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US-08-842-842-6
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US-09-052-521C-1
                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS; LOCATION: (158)..(1105) US-09-052-521C-1
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RESULT 13
US-07-968-971A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
                                                                                                                                                                                                                                                                                              Matches 125; Conservative
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PRIOR FILING DATE: 1997-(
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1997-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       750 TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 809
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Local Similarity 70.2%;
es 125; Conservative
                                                                       810 ACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCT 867
                                                                                                           122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
                                                                                                                                                 750 TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 809
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                                                                                                                                                                                     68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
                                                                                                                                                                                                                                                          8 CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACA 67
                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                h 39.6%; Score 80.8; DB 4; Length 2295; Similarity 70.2%; Pred. No. 3.8e-20;
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Sequence 5, Application US/07968971A Patent No. 5455167
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                                                                                                                                      Matches
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Huw Maelor Davies
TITLE OF INVENTION: Medium-Chain Thioesterases
TITLE OF INVENTION: In Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple Macintosh (
OPERATING SYSTEM: Macintosh (
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 07/82
APPLICATION NUMBER: 07/82
APPLICATION STATE: 22-0AN-1992
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 21-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-JAN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
1301 AATATCAGAAAAATAACTCAATGAGTCAAGGTTAT 1335
                                                                  1241 CAGAATCATGGCCTGTGGTTTTAGATATATATCCAAAATTGTCCTATAGTCAAGAAACTT 1300
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ETILING DATE: 7-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/782,263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US92/04332
                                                                                                 10 CATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATG 69
                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME:
                                 70 ACTITCAGCAACGGAAAACTAAGAGTCAAAGGCAT 104
                                                                                                                                                      Local Similarity
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                                                                                                                                                        14.4%; Score 29.4; DB 1; Length 1461; 56.8%; Pred. No. 0.4;
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; Sequence 47, Application US/07824247

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US-07-824-247-47

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1301 AATATCAGAAAAATAACTCAATGAGTCAAGGTTAT 1335
                                              1241 CAGAATCATGGCCTGTGGTTTTAGATATATATCCAAAATTGTCCTATAGTCAAGAAACTT 1300
                                                                                                                                                                         MOLECULE TYPE: PCR product from mRNA template
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                      TELEPHONE: 916-753-6313
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                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 26-APR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/6
FILING DATE: 27-FEB-1991
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
07/662,007
                        70 ACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCAT 104
                                                               10 CATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/71
FILING DATE: 21-MAY-1991
PRIOR APPLICATION DATA:
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                                                                                                                               Local
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/620,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/
FILING DATE: 25-APR-1991
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FILING DATE: 24-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macinto:
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STATE: Cali
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                                                                                                                  54;
                                                                                                                            Similarity
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                                                                                                                   Score 29.4; DB 1; Length 1461; Pred. No. 0.4;
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Best Local Similarity
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US-08-142-473A-7
                                                                                                                                                                                                                                                                                                              TELEFAX: 916-753-1510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08142473A Patent No. 5639790 GENERAL INFORMATION:
1301 AATATCAGAAAAATAACTCAATGAGTCAAGGTTAT 1335
                                                        1241 CAGAATCATGGCCTGTGGTTTTAGATATATATCCAAAATTGTCCTATAGTCAAGAAACTT 1300
                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1461 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 21-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/
FILING DATE: 7-0CT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 24-OCT-
                              70 ACTITICAGCAACGGAAAACTAAGAGTCAAAGGCAT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                     10 CATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 07/824,247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Macintosh IIci
OPERATING SYSTEM: Macintosh 7
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
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APPLICANT: Davies, Huw Maelor
TITLE OF INVENTION: Plant Thioesterases
                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Donna E. Scherer
REGISTRATION NUMBER: 34
NAME: Carl J. Schwedler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            TELEPHONE: 916-753-6313
TELEFAX: 916-753-1510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/142,473A
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                                                                                                                                     54;
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                                                                                                                                   Conservative
                                                                                                                                                                                                                                linear
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1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vombER: PCT/US92/04332
21-MAY-1992
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                                                                                                                                                                                                                                             single
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                                                                                                                         0; Mismatches 41; Indels
                                                                                                                                        Score 29.4; DB 1; Length 1461; Pred. No. 0.4;
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us-09-880-457-1_copy_543_746.rni

Search completed: December 8, 2002, 17:28:32 Job time : 17.9188 secs

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OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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                                                                                                                                                                                                                           Result
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                                                                                                                                                                                                                                                                   pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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178
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Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                   Match Length DB
                                                                                                                                                                                                                                                                                                             Published_Applications_AA:*
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Listing first 45 summaries
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 46.6
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                                                     0 US-09-813-329-7

0 US-09-871-856-13

US-10-017-910-2

10S-09-779-050A-14

US-09-877-650-11

0 US-09-871-856-11

0 US-09-871-856-11

0 US-10-017-910-4

10 US-09-911-777-8
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US-09-880-457-5
US-09-880-457-6
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US-09-877-650-13
  US-09-924-841-5
US-09-924-841-9
US-09-801-368-334
US-10-119-714-1
US-09-925-302-760
                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                Sequence 7, Appli
sequence 13, Appl
sequence 2, Appli
sequence 14, Appl
                                                                                                                                                                                                                         Description
                            Sequence 8, Appli
Sequence 5085, Ap
Sequence 5, Appli
Sequence 9, Appli
Sequence 334, Appli
                                                                               Sequence 11, Appl
Sequence 4, Appli
                                                                                                        Sequence 11
                                                                                                                                                           Sequence 13,
                                                                                                                                                                      Sequence 15,
                                                                                                                                                                                 Sequence
                                                                                                                                                                                   Sequence 4, Appli
Sequence 5, Appli
Sequence 6, Appli
        Sequence 1, Appli
Sequence 760, App
                                                                                                      , Appl
                      Appli
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220 221 221 222 223 223 222 222 222 223 223
54 54 54 54 54 55 52 53 53 53 53 53 53 53 53 53 53 53 53 53
14.5 14.5 14.5 14.5 14.5 14.5 14.5 14.5
57 333 146 146 261 261 261 27 204 77 204 764 764 764 764 764 764 764 764 764 76
10 10 10 10 10 10 10 10 10 10 10 10 10 1
US-09-864-761-42649 US-09-779-050A-10 US-09-73-455-16 US-09-34-455-16 US-09-842-745A-2 US-09-864-761-39850 US-09-864-761-39850 US-09-864-761-39850 US-09-864-761-39850 US-09-815-242-12814 US-09-815-242-12814 US-09-815-242-12814 US-09-815-242-12814 US-09-815-242-12814 US-09-815-242-12814 US-09-815-242-12814 US-09-815-242-12814 US-09-815-242-15814 US-09-815-242-15814 US-09-815-242-15814 US-09-815-242-15814 US-09-943-446-9 US-10-027-806-12 US-09-354-446-9 US-09-354-446-9 US-09-354-446-9 US-09-354-446-9 US-09-354-446-9 US-09-354-446-9 US-09-354-446-9 US-09-354-463-36 US-09-354-463-36 US-09-992-598-422 US-09-992-598-422 US-09-992-598-422
Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 16, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 39850, Appli Sequence 4, Appli Sequence 4, Appli Sequence 12447, A Sequence 12447, A Sequence 5522, Ap Sequence 5522, Appli Sequence 17, Appli Sequence 56, Appli Sequence 9, Appli Sequence 9, Appli Sequence 10, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 16, Appli Sequence 17, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 18, Appli Sequence 19, Appli

ALIGNMENTS

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US-09-880-457-4
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                                                                                                                                                                                                                                                                                                                                                                                               US-09-880-457-4
; Sequence 5, Application US/09880457
; Patent No. US20020106728A1
; GENERAL INFORMATION:
; APPLICANT: Pan, James
; APPLICANT: Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 4
                                                                                                                                                                                                                                               Вþ
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                                                                                                                                                                          밁
                                                                                                RESULT 2
US-09-880-457-5
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APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
APPLICANT: Wood, Wood Methods of Use
APPLICANT: Wood, Wood Methods of Use
APPLICANT: Wood, Wood Methods of Use
FILE REFERENCE: P3871R1
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                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 87
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                               Local
                                                                                                                                                                        80 WCNLRIIH 87
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68; Conserv
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RESULT 4
US-09-779-050A-15
; Sequence 15, Application US/09779050A
; Patent No. US20020160416A1
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: SEQ ID NO 5
: LENGTH: 94
: TYPE: PRT
: ORGANISM: HOMO Sapiens
US-09-880-457-5
CURRENT APPLICATION NUMBER: US/09/779,050A
                     APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM THE FAMILY
FILE REFERENCE: A-570B
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
CURRENT FILING DATE: 2001-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09880457 Patent No. US20020106728A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
                                                                                                                                                                                                                                  61 WCNLRII 67
                                                                                                                                                                                                                                               80 WCNLRSV 86
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                                                                                                                                                                                                                                                                                                                                 65;
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                                                                                                                                                                                                                                                                                                                             96.0%; Score 358; DB 10; Length 95; 97.0%; Pred. No. 6.7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.0%;
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    Mismatches

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WOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-877-650-13
                 Best Local Similarity 60.0
Matches 36; Conservative
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LENGTH: 160
TENGTH: 160
TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-050A-15
                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-877-650-13
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                                                                                                                                                                                       TELEPHONE: (206)587-04:
TELEPAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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PRIOR APPLICATION NUMBER: 60/7
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/995,659

FILING DATE: 1997-12-22

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NEWLY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                           NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Un-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Anderson, Dirk M.
                                                                                                                                                                      LENGTH: 317 amino acids
                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: WA
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 47.7%; Score 178; DB 9; Length 317; 60.0%; Pred. No. 2.7e-15; ative 5; Mismatches 17; Indels
                                                                                                                                                                                                                                              (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunex Corporation, Law Department
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Patent No. US20020012968A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bristol-Myers Suibb Company
TITLE OF INVENTION: NO. US20020012968A161 Drosophila Tumor Necrosis Factor Class Mole
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-03-20 FRIOR APPLICATION NUMBER: 60/190,816 PRIOR FILING DATE: 2000-03-21 NIMBER OF CENTRAL PRIOR FILING DATE: 2000-03-21 NIMBER OF CENTRAL PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT FILING DATE: 2001-03-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLVANICFRHHETSGDLATEYLQL 238
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                                                                                                                                                                                                                                                                                                               COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power Macintosh
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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Galibert, Laurent
Maraskovsky, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Receptor Activator of NF-kappaB
TELECOMMUNICATION INFORMATION:
                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                  APPLICATION NUMBER: 08/996,139
FILLING DATE: <UNknown>
APPLICATION NUMBER: USSN 08/813,509
FILLING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILLING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/871,856 FILING DATE: 31-May-2001 CLASSIFICATION: <Unknown>
                 NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
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Pred. No. 2.7e-15;
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US-10-017-910-2
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                                  Query Match
Best Local Similarity
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                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hackensack
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                 Conservative
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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-017-910-2
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TELEPAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 47.7%;
Local Similarity 60.0%;
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/447,035
FILING DATE: 1999-11-22
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/017,910
FILING DATE: 14-Dec-2001
                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steinman, Ralph
TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                        TELEFAX: 201-343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 317 amino acids
                                                                                                                                                                                        LENGTH: 245 amino acids
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Wong, Brian
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46.6%; Score 174; DB 9;
58.3%; Pred. No. 6.4e-15;
tive 5; Mismatches 18
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Pred. No. 2.7e-15;
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                                       Length 245;
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  Indels
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RESULT 10
US-09-877-650-11
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US-09-779-050A-14
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PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Best Local :
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APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM THE FAMILY
FILE REFERENCE: A-570B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/779,050A CURRENT FILING DATE: 2001-02-12
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                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98101
COMPUTER READABLE FORM:
                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 56.7 34; Conservative
                          REGISTRATION NUMBER: 34,0
REFERENCE/DOCKET NUMBER:
                                                               NAME: Perkins, Patricia Anne
                                                                                                      APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                     APPLICATION NUMBER: 08/995,659 FILING DATE: 1997-12-22
                                                                                                                                                                                                                                            FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/877,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
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Pred. No. 6.8e-15;
6; Mismatches 18
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                                                                                                   ; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-871-856-11
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US-09-871-856-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09871856 Patent No. US20020081720A1 GENERAL INFORMATION:
                                          Query Match
Best Local Similarity
                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206)233-064
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 SHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL 215
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patticia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 31-May-2001 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.
                                                                                                                                                                               TYPE: amino acids
                                                                                                                                                                                                                                                               TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/871,856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Microsoft Word for Power
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 294 amino acids
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maraskovsky, Eugene
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56.78;
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                                          46.18;
56.78;
                                                                                                                                                                                                                                                                                     (206)587-0430
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                                          Score 172; DB 10;
Pred. No. 1.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 172; DB 9;
Pred. No. 1.4e-14;
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                        Mismatches
                                                                                                                                                                                                                                                                                                                        2851-A
                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macintosh
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                                                             Length 294;
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                      Indels
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Patent No. US20020159970A1
GENERAL INFORMATION:
APPLICANT: Choi, Yongwon
                                                                                                                                                                                                                                                                                                                 US-09-911-777-8
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                                                                                                                                                                                        Sequence 8, Application US/09911777
Patent No. US20020037852A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                APPLICANT: BIOGEN, INC. APPLICANT: APOTECH S.
                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 SHKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 46.1%;
Local Similarity 56.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/017,910
FILING DATE: 14-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

CHASTION TO THE TOP TO THE TOP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 09/447,035 FILING DATE: 1999-11-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 316 amino acids
                                         APOTECH S.A.
BROWNING, Jeffrey
AMBROSE, Christine
    MACKAY, Fabienne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steinman,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ralph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 172; DB 9; Length 316; Pred. No. 1.6e-14;
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                                         Matches
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; ORGANISM: Homo Sapien US-09-911-777-8
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                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/191.078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
                                                                               ; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-5085
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SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/117,169
PRIOR ETLING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 60/143,228
PRIOR ETLING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: PCT/US00/01788
                                                                                                                                         NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5085
LENGTH: 813
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NUMBER OF SEQ ID NOS: 22
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Proxaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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CURRENT FILING DATE: 2001-03-21
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                  Best
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 50/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-12-22
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                Local Similarity
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19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carr, Grant J.
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Trawick, John D.
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Conservative
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                     17.0%; Score 63.5; Di 28.8%; Pred. No. 3.5;
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11; Mismatches
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                                              DB 10;
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       23;
                                                 Length 813;
         Indels
           13; Gaps
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GENERAL INFORMATION:

APPLICANT: Dilley, David R

APPLICANT: Wang, Zhenyong

APPLICANT: Wang, Zhenyong

APPLICANT: Warner, Toni M

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
FILE REFERENCE: MSU41-453

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US/09/924,841

PRIOR PILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US/09/413,231

PRIOR FILING DATE: 1999-10-06

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: modified IPNS
NAME/KEY: MUTAGEN
LOCATION: (210)

US-09-924-841-5
Search completed: December 8, 2002, 19:36:16 Job time: 11.0903 secs
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US-09-924-841-5
Sequence 5, Application US/09924841
Patent No. US20020127633A1
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                                                                                    120 GTPMHEVNLW 129
                                                                                                                             52 GLTLQDLQLW 61
                                                                                                                                                           60 NEFHGAMTDQEKHDLAIHAYNPDNPHVRNGYYKAVPGRKAVESFCYLNPDFGEDHPMIAA 119
                                                                                                                                                                                                  1 HEAHKTSLSSWKHD------ODWANVSNMTFS--NGKLRVKGIYYRNADICSRHRVTSA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        771 LGIQNL 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           711 TAYLQYKPDADWNNRLQATFFDSKDYRLDGVESFGRRQVSTYTTVDLVSQYRITPDDQLS 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 LTLQDL 58
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OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
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                                                                                                                                                                                                                                    NO.
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                     Score
                                                                    180.5
180.5
180.5
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length: 2000000000
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1 MAILTLSLOLILLLIPSISH......TSAGLTLQDLQLWCNLRIIH 87
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100.0
96.7
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Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                     Match Length DB
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Listing first 45 summaries
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0 US-09-880-457-5

0 US-09-880-457-5

0 US-09-779-050A-15

0 US-09-877-650-13

10 US-09-871-856-13
            10 US-09-871-556-11

US-10-017-910-4

10 US-09-911-77-8

10 US-09-815-242-5085

10 US-09-924-841-5

10 US-09-924-841-9

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10 US-09-792-2008-22

10 US-09-853-533A-2
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US-09-779-050A-14
US-09-877-650-11
     US-10-133-178-4
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                                                                                                                                           Sequence 15, Appl
Sequence 17, Appli
Sequence 7, Appli
Sequence 13, Appl
                             Sequence 2, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 4, Appli
Sequence 8, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 9, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                               Description
                                                                                                                                                                                     Sequence 4, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 15, Appl
       Sequence 22, Appli
Sequence 2, Appli
Sequence 4, Appli
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12.5 12.5 12.4 12.4 12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3
441 720 333 753 484 878 878 878 146 1146 1151 157 821 1151 1151 1151 1151 1151 1151 1151
10 10 10 10 10 10 10 10 11 10 10 10 10 1
US-09-815-242-4986 US-09-801-368-176 US-09-925-302-760 US-09-925-301-866 US-10-060-332-2 US-09-79-050A-10 US-09-79-050A-10 US-09-842-745A-2 US-09-842-745A-2 US-09-842-761-42649 US-09-764-868-883 US-09-861-368-266 US-09-801-368-266 US-09-801-368-326 US-09-801-367-4 US-09-801-367-2 US-09-801-37-2 US-09-801-367-2 US-09-801-367-2 US-09-801-367-2 US-09-801-367-2 US-09-801-368-3128-4 US-09-801-368-3 US-09-801-368-
sequence 176, App Sequence 176, App Sequence 10, Appl Sequence 340, App Sequence 366, App Sequence 2, Appli Sequence 10, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appli Sequence 2, Appli Sequence 266, App Sequence 2766, App Sequence 2766, App Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 119, Appli Sequence 119, Appli Sequence 119, Appli Sequence 119, Appli Sequence 110, Appli Sequence 21, Appli Sequence 12447, Appli

ALIGNMENTS

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RESULT 1
US-09-880-457-4
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Sequence 6, Application US/09880457
Patent No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
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APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
TITLE OF INVENTION: FOR THE TREATMENT OF THE TREATMENT O
                                                                                                                                                                                                                                                  RESULT 2
US-09-880-457-6
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LENGTH: 87
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/212,901 PRIOR FILING DATE: 2000-06-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ICSRHRVTSAGLTLQDLQLWCNLRIIH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ICSRHRVTSAGLTLQDLQLWCNLRIIH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 100.0%; Score 455; DB 10; al Similarity 100.0%; Pred. No. 1.3e-49; 87; Conservative 0; Mismatches 0;
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US-09-779-050A-15
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CURRENT ETLING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 5
LENGTH: 94
TYPE: PRT
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                                                                                               Sequence 15, Application US/09779050A Patent No. US20020160416A1 GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/09/779,050A
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                    TITLE OF INVENTION: RECEPTOR FROM THE FAMILY FILE REFERENCE: A-570B
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                                                                 APPLICANT: BOYLE, WILLIAM APPLICANT: HSU, HAILING
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09880457 Patent No. US20020106728A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 96.7%;
Best Local Similarity 97.7%;
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SEQ ID NO 6
LENGTH: 95
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TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
FILE REFERENCE: P2871R1
                                                                                                                                                                                                                       61 ICSRHRVTSAGLTLQDLQLWCNLRSV 86
                                                                                                                                                                                                                                          61 ICSRHRVTSAGLTLQDLQLWCNLRII 86
                                                                                                                                                                                                                                                                                1 MAILMESEQLILLEPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVKGIYYRNAD 60
                                                                                                                                                                                                                                                                                                 1 MAILTLSLQLILLLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVKGIYYRNAD 60
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                                                                                                                                                                                                                                                                                                                                                                 1 Similarity 96.5
83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84; Conservative
                                                                                                                                                                                                                                                                                                                                                     95.4%; Score 434; DB 10; Length 94; 96.5%; Pred. No. 5.6e-47; rative 1; Mismatches 2; Indels
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US-09-877-650-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-779-050A-15
                                                                  TELEPHONE: (206)587-0430
TELEPAX: (206)233-0644
TELEPAX: (206)233-0644
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-02-12 PRIOR APPLICATION NUMBER: 60/181,800 PRIOR FILING DATE: 2000-02-11 NUMBER OF SEQ ID NOS: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 160
TYPE: PRT
     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                         NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 IPSGS---HKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA;
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Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/995,659
FILLING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILLING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILLING DATE: 23 DECEMBER 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Immunex Corporation STREET: 51 University Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.7%; Score 180.5; DB 9; 59.7%; Pred. No. 2.9e-15;
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US-09-871-856-13
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CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 317
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/09871856 Patent No. US20020081720A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09813329 Patent No. US20020012968A1
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TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole
TITLE OF INVENTION: Variants Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: D0016.np
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-MAY-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                Galibert, Laurent
Maraskovsky, Bugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                      STATE: WA
                                                                                                                                                                                                                                                         ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
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                                                                                                                                                                                                                                      CITY: Seattle
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Pred. No. 7e-15;
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US-10-017-910-2
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                                                                                                                                                    COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/017,910
FILING DATE: 14-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steinman, Ralph
TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION
               ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                     APPLICATION NUMBER: US 09/447,035 FILING DATE: 1999-11-22
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REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 411 Hackensack Avenue, 4th Floor CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New Jersey
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59.7%;
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RESULT 10
US-09-817-650-11
; Sequence 11, Application US/09877650
; Patent No. US20020169117A1
; GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BOYLE, WILLIAM APPLICANT: HSU, HAILING
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INFORMATION FOR SEQ ID NO: 2:
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Local Similarity 55.4%;
es 36; Conservation
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               CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                       Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                  APPLICANT: Anderson, Dirk M.
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CITY:
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TYPE: amino acid
TOPOLOGY: linear
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     Seattle
                                                                                                                   Galibert, Laurent
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58.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 176; DB 9;
Pred. No. 1.1e-14;
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Pred. No. 1.6e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 160;
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-877-650-11
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US-09-871-856-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 DYLQL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 SIPSGSHKYTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: PORKINS, PATRICIA Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 QDLQL 79
COMPUTER: RADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.!
SOFTWARE: Microsoft Word for Power Macintosh (
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power Macintosh
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                                                                                                                                                              COUNTRY: USA
ZIP: 98101
                                                                                                                                                                                                                       STATE: WA
                                                                                                                                                                                                                                          CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 294 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                         ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 08-Jun-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/877,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                   Maraskovsky, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (206)587-0430
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-871-856-11
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US-10-017-910-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 SIPSGSHKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 QDLQL 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Choi, Yongwon
Wong, Brian
                                                                                                                                           CORRECTION TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/017,910

FILING DATE: 14-Dec-2001

CLASSIFICATION: CUNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steinman, Ralph
TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY
                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/447,035
FILING DATE: 1999-11-22
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 294 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 176; DB 10; Length 294; Pred. No. 2.3e-14; 6; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                      ; Sequence 5085, Application US/09815242
                                          US-09-815-242-5085
                                                                RESULT 14
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US-10-017-910-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                       ; TYPE: PRT ; ORGANISM: Homo Sapien US-09-911-777-8
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/911,777
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/117,169
PRIOR FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 60/143,228
PRIOR APPLICATION NUMBER: 60/143,228
PRIOR APPLICATION NUMBER: PCT/US00/01788
PRIOR APPLICATION NUMBER: PCT/US00/01788
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 8, Application US/09911777
Patent No. US20020037852A1
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BIOGEN, INC. APPLICANT: APOTECH S. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                  Matches
                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: BAFF, Inhibitors Thereof and Their Use TITLE OF INVENTION: in the Modulation of B-Cell Response FILE REFERENCE: A070 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 SIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT 232
                                                                                                                                                                                                                                                                                   LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 DYLQL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 SISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 QDLQL 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                         15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVKGIYYRNADICSRHRVTSAGLTL 74
57 EYLQL 61
                                    75 QDLQL 79
                                                                      15 IPSGS---HKVSLSSWYHDRGWGKISNM-----YANICFRHHETSGDLAT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BROWNING, Jeffrey
AMBROSE, Christine
MACKAY, Fabienne
TSCHOPP, Jurg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 316 amino acids
                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCHNEIDER, Pascal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APOTECH S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.7%;
                                                                                                                                                                      25.3%; Score 115; DB 10; Length 109; 43.1%; Pred. No. 2.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibitors Thereof and Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 176; DB 9;
Pred. No. 2.5e-14;
                                                                                                                                                        4; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                  18;
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GENERAL INFORMATION: Patent No. US20020061569A1

APPLICANT: Haselbeck, Robert

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APPLICANT: Dilley, David R
APPLICANT: Kadyrzhanova, Dina K
APPLICANT: Wang, Zhenyong
APPLICANT: Wanner, Toni M
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
FILE REFERENCE: MSUA1-453
CURRENT PILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US/09/924,841
CURRENT FILING DATE: 1999-10-06
NUMBER OF SEQ ID MOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITA, 011A
CURRENT APPLICATION NUMBER: U$/99/815,242
CURRENT APPLICATION NUMBER: U$/99/815,242
PRIOR APPLICATION NUMBER: 60/2191,078
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09924841
Patent No. US20020127633A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5085
LENGTH: 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
     ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       711 TAYLQYKEDADWNNRLQATFFDSKDYRLDGVESFGRRQVSTYTTVDLVSQYRITPDDQLS 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 TSLSSWKHDQDWANVSNMTFSNGK-LRVKGI-----YYRNADICSRHRVT---SAG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity es 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zyskind, Judith W. Wall, Daniel Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.0%; Score 63.5; DB 10; Length 813; 28.8%; Pred. No. 7.4; rative 11; Mismatches 23; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Indels 13; Gaps
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                                                                                                                                                                                                                                  US-09-924-841-5
                                                                                                                                                  Best Local Similarity 24.0 Matches 18; Conservative
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: modified IPNS NAME/KEY: MUTAGEN LOCATION: (210) OTHER INFORMATION: Glu210 in native IPNS modified to Arg
115 PMIAAGTPMHEVNLW 129
                                    66 RVTSAGLTLQDLQLW 80
                                                           55 LQDVVNEFHGAMTDQEKHDLAIHAYNPDNPHVRNGYYKAVPGRKAVESFCYLNPDFGEDH 114
                                                                                             15 IPSISHEAHKTSLSSWKHD------QDWANVSNMTFS--NGKLRVKGIYYRNADICSRH 65
                                                                                                                                      13.5%; Score 61.5; DB 10; Length 24.0%; Pred. No. 4.1; ative 12; Mismatches 36; Indels
                                                                                                                                                                             Length 329;
                                                                                                                                    9; Gaps
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Job time : 13.9097 secs Search completed: December 8, 2002, 19:36:15

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OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
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204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350425 segs, 194966369 residues
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Listing first 45 summaries
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Copyright (c) 1993 - 2002 Compugen Ltd.
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6674.007 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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30 29.4 29.4	31.2 31.2 31.2	61 31.2 31.2 31.2	80.8 80.8	194 96.4 96.4 93.2	Score 204 194
14.7 14.4 14.4	15.3 15.3	15.3 15.3	39. 66. 66.	95.1 47.3 47.3 45.7	Match 100.0 95.1
30 409 454	3073 3073 3073	493 985 985	1630 1630 2237	2412 954 954 1823	Query Match Length 100.0 1161 95.1 1186
10 10	10	10	9019	10 10	DB
US-09-880-457-8 US-09-783-590-1953 US-09-864-761-14164	US-09-867-701-10910 US-09-920-300A-1690 US-10-033-528-1690	US-10-040-739-93 US-10-040-739-93 US-09-920-300A-1691 US-10-033-528-1691	US-09-877-650-10 US-09-871-856-10 US-10-017-910-3	US-09-880-457-2 US-09-877-650-12 US-09-871-856-12 US-10-017-910-1	ID US-09-880-457-1 US-09-880-457-3
Sequence 6, Appri Sequence 1953, Ap Sequence 14164, A	0 1 1 1	Sequence 93, Appl Sequence 1691, Ap Sequence 1691, Ap) w t "

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44 44 5	41 42	40 40	36	34 35	ω ω Α ω	υ U U	30	29	2 6	26	25	24	23	22	21	20
27 27 27	27.2 27.2	27.6	27.6	27.6 27.6	27.6	27.8	27.8	27.8	28.2	28.2	28.2	28.2	28.2	28.6	28.6	29.4
13.2 13.2 13.2	13.3 13.3		 		13.5						13.8			14.0	14.0	14.4
27 280 9542	817 2000	1873 1873	008 008	608 808	809	65237	2048	666	2000	477	477	477	477	1365	1365	2244
10 10	9	10	10	10	10	10	10	10		10	10	10	10	10	10	10
US-09-880-457-7 US-09-294-093B-5098 US-09-764-847-1809	US-09-809-545A-7 US-09-938-842A-4387	US-09-834-975-756 US-09-834-975-757	US-09-822-827-193 US-09-115-453-193 US-09-935-943-7	US-09-780-669-193	US-09-759-143-193	US-09-933-267A-1	US-09-764-847-1468	US-09-764-864-590	US-09-938-842A-4251	US-09-115-453-92	US-09-030-606-92	US-09-780-669-92	US-09-759-143-92	US-09-815-242-8196	US-09-815-242-4243	US-09-764-864-153
Sequence /, Appli Sequence 5098, Ap Sequence 1809, Ap	Sequence 1, Appli Sequence 4387, Ap	Sequence 756, App Sequence 757, App	sequence 193, App Sequence 193, App Sequence 7, Appli	sequence 193, App sequence 193, App	sequence 193, App	Sequence 1, Appri Sequence 285, App	Sequence 1468, Ap	Sequence 590, App	Sequence 4251, Ap	sequence 92, Appl	sequence 92, Appl	Sequence 92, Appl	Sequence 92, Appl	Sequence 8196, Ap	Sequence 4243, Ap	

ALIGNMENTS

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; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-880-457-1
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US-09-880-457-1
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09880457 Patent No. US20020106728A1
                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 204; DB 10; Best Local Similarity 100.0%; Pred. No. 1.5e-60; O: Mismatches 0;
                                                                                                                                                                                                                                                                          Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use TITLE OF INVENTION: for the Treatment of Body Weight Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: P2871R1
                                                                                                                                                                                                   723 TGGTGTAATTTGAGAATCATTCAC 746
                             181 TGGTGTAATTTGAGAATCATTCAC 204
                                                                                                                                                                 61 TCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGGAATGCC 120
                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                               Length 1161;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                  Gaps
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В
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                                                                                                                                                                                           : NUMBER OF SEQ ID NOS: 9
: SEQ ID NO 2
: LENGTH: 2412
: TYPE: DNA
: ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-880-457-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA; ORGANISM: Homo sapiens US-09-880-457-3
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09880457
Patent No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-880-457-3
                                                                                              Matches
                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                          FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Milliam I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
LENGTH: 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      684 TGGTGTAATTTGAG 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564 TCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCC 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        504 CATGAGGCTCATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTC 563
                                                                                                                  Loca 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CATGAGGCTCATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAAACGTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 95.1%; Score 194; DB 10; Length 1186; Local Similarity 100.0%; Pred. No. 4.2e-57; es 194; Conservative 0; Mismatches 0; Indels 0.
                                                                                                 194;
                                                                                                                Similarity
                                                                                              Conservative
                                                                               95.1%; Score 194; DB 10; Length 2412; 100.0%; Pred. No. 5.6e-57; 101.0%; Mismatches 0; Indels 0
                                                                                      0;
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US-09-877-650-12
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                           TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 TGGTGTAATTTGAG 194
           SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                       FEATURE:
                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 2852-A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
                                                                                                                                                                               ANTI-SENSE: NO
                                                                                                                                                                                                HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                    LOCATION:
                                                                                    CLONE: huRANKL (full length)
                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                              NAME/KEY: CDS
                                                                                                           LIBRARY:
                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                        LENGTH: 954 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
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Sequence 12, Application US/09871856

Patent No. US20020081720A1

GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                               TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         591 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     651 TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 47.3%; Score 96.4; DB 9; Length 954; Local Similarity 74.5%; Pred. No. 1.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        711 ACTA 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 2851-A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                           TOPOLOGY: linear MOLECULE TYPE: cDNA
                  ORIGINAL SOURCE:
                                           ANTI-SENSE: NO
                                                             HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/871,856 FILING DATE: 31-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/996,139
                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                       NAME: Perkins, Patricia Ann
REGISTRATION NUMBER: 34,693
                                                                                                                                                                      LENGTH: 954 base pairs
                                                                                                                                                                                                                                                     TELEPHONE: (206)587-0430
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunex Corporation, Law Department
                                                                                                                                                                                                                                                                                                                                         Patricia Anne

 Mismatches

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US-09-871-856-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
              TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTTGGGCCAAGATCTC 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               591 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        711 ACTA 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steinman, Ralph
TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                        REFERENCE/DOCKET NUMBER: 600-1-200 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: <Unknown>
                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                FILING DATE: 14-Dec-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                       APPLICATION NUMBER: US 09/447,035 FILING DATE: 1999-11-22
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/017,910 FILING DATE: 14-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                 NAME: Jackson Esq., David REGISTRATION NUMBER: 26,74
LENGTH: 1823 base pairs
                                                                          TELEFAX: 201-343-1684
                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi, Yongwon
Wong, Brian
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                                                                                              201-487-5800
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Pred. No. 1.4e-23;
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                                                                                                                                                     26,74
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US-09-877-650-10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435 TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTGGGGGTAAGATCTC 374
                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/995,659

FILING DATE: 1997-12-22

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997
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                  NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                          COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
                                                                                       APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Anderson, Dirk M. Galibert, Laurent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: cDNA
_ TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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73.4%;
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US-09-871-856-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589 ACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  529 TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 588
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                 APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
                                                                                                                                                                                                            COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 CTCATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCCAACA 67
                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                        ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Anderson, Dirk M.
Galibert, Laurent
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
NAME: Perkins, Patricia Anne
                                                                                                                                                                              APPLICATION NUMBER: US/09/871,856 FILING DATE: 31-May-2001
                                                                                                                                                                  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                           COUNTRY
                                                                                                                                                                                                                                                                                                                                                                         STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE: RANKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                       : USA
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                                                                                                                                                                                                                                                                                                                                                                                                                Immunex Corporation, Law Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.6%; Score 80.8; DB 9; Length 1630; 70.2%; Pred. No. 4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .884
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REFERENCE/DOCKET NUMBER: 2851-A

REGISTRATION NUMBER: 34,693

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US-10-017-910-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10017910 Patent No. US20020159970A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469 CCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACA 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 39.6%;
Local Similarity 70.2%;
es 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACA 67
                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   Steinman, Ralph
TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC AC
                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Choi, Yongwon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: cDNA
                                   APPLICATION NUMBER: US/10/017,910
FILING DATE: 14-Dec-2001
CLASSIFICATION: <Unknown>
APPLICATION NUMBER: US 09/447,035
                                                                                                                                                                                                                          ZIP:
                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                           STATE: New Jersey
                                                                                                                                                                                                                                                                                   CITY: Hackensack
                                                                                                                                                                                                                                                                                               STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 3..884
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                                                                                                                                                                                                                            07601
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                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                 METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 80.8; DB 10;
Pred. No. 4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                              : NUMBER OF SEQ ID NOS: 9
: SEQ ID NO 9
: LENGTH: 61
: TYPE: DNA
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                                                                                   Matches 61;
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                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                              APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, William I.

TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                              OTHER INFORMATION: Cloning oligonucleotide
                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   674 CCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACA 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            794 ACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCT 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 ACATTIGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
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                 75 CAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATTTGCTCTCG 134
                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
1 CAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATTTGCTCTCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 CTCATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGGCAAACGTCTCCAACA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 142..1092
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2237 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1999-11-22
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA
                                                                              29.9%; Score 61; DB 100.0%; Pred. No. 6. tive 0; Mismatches
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70.2%;
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Pred. No. 4.6e-18;
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                                                                                                  DB 10; I
. 6.5e-12;
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                                                                              0;
                                                                                                                   Length 61;
                                                                              Indels
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RESULT 12
US-09-920-300A-1691
; Sequence 1691, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 93: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               317 AAACAACGAGCCAAGCTCCAGAAAATGTTGCCCCAAGCTGGAAGAAGAGTTGAAGGCACGA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 A 61
                                                                                                                                                                                    71
                                                                                                                                                                                                                                                                   11 ATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCCAAACGTCTCCAACATGA 70
                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPAX: (617) 876-5851
RMATION FOR SEA TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,739
FILING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 93:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jacobs, Kenneth
                                                                                                                                                                     CTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATTGCCGACATT 126
                                                                                                                                                ATTGAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATGGGCAGAAATT 432
                                                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 493 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/036,520 FILING DATE: 03-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Cambridge
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Merberg, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LaVallie, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCoy, John
                                                                                                                                                                                                                                                                                                                                   15.3%;
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                                                                                                                                                                                                                                                                                                                                                    Length 493;
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                                                                                                                                                                                                                                                                                                                0
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APPLICANT: Meagher, Madutation applicant: Xu, Jiangchun Applicant: Xu, Jiangchun Applicant: Secrist, Heather Applicant: Secrist, Heather TIILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1691
LENGTH: 985
TYPE: DNA
ORGANISM: Homo sapiens
US-09-920-300A-1691
15.3%; Score 31.2; DB 10; Length 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
INTELOF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILLING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1691
LENGTH: 985
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                                                                                                                      US-09-867-701-10910
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                                                                                                                                          RESULT 14
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                                              GENERAL INFORMATION:
                                                                   Sequence 10910, Application Patent No. US20020132237A1
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 63; Conserv
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APPLICANT: Meagher, Madeleine Joy
APPLICANT: Aglate, Paul A. APPLICANT: Jones, Robert
                                                                                                                                                                                                              447 ATTGAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATGGGCAGAAATT
                                                                                                                                                                                                                                                                                                          387 ANACHACGAGCCCAAGCTCCAGAAAATGCTGCCCAAGCTGGAAGAAGAGTTGAAGGCACGA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 ATTGAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATGGGCAGAAATT 502
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31.2; DB Pred. No. 0.37;
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APPLICANT:

Harlocker, Susan L.

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; TYPE: DNA; ORGANISM: Homo sapiens US-09-867-701-10910
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US-09-920-300A-1690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.497
CURRENT APPLICATION UNMEER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
UNMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10910
LEBGTH: 3073
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Matches 63; Conservative (
Search completed: December 8, 2002, 19:38:04 Job time : 18.9188 secs
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1690
LENGTH: 3073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: King, Gordon E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 1690, Application US/09920300A Patent No. US20020136728A1
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
FILE REFERENCE: 210121.547
                                                                                                                                                                                                                                     Matches
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                                                                                                                                                     11 ATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGA 70
                                                                                                                                                                                            11 ATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGA 70
                                                                                                               71 CTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATT 126
                                                                                                                                                                                                                                 Match 15.3%; Score 31.2; DB 10; Length 3073; Local Similarity 54.3%; Pred. No. 0.6; es 63; Conservative 0; Mismatches 53; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meagher, madeleine Joy
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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                 Database :
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           December 8, 2002, 17:18:27; Search time 15.2491 Seconds (without alignments) 6674.007 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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261
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Listing first 45 summaries
: //cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq: *
:/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq: *
:/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq: *
:/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq: *
:/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq: *
:/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq: *
:/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq: *
:/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq: *
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:/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq: *
:/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq: *
:/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq: *
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 18 c 19	12 13 15 16	c 110	654321	Result
31.2 30.8 30.4	31.2 31.2 31.2 31.2	95.6 95.6 61	261 251 251 249.4 121.2 121.2	Score
12.0 11.8 11.6	12.0 12.0 12.0 12.0	36.6 36.6 12.4 12.6	100.0 96.2 95.6 46.4 45.4	Query Match
3073 30310 53226	493 985 985 3073	1630 1630 2237 61 454	1161 1186 2412 954 954 1823	Query Match Length DB
12 10	10 12 10	10	10 10 10 9	DB
US-10-033-528-1690 US-09-800-631-96 US-09-818-264-3	US-10-040-739-93 US-09-920-300A-1691 US-10-033-528-1691 US-09-867-701-10910 US-09-920-300A-1690	US-09-877-550-10 US-09-871-856-10 US-09-881-950-10 US-10-017-910-3 US-09-880-457-9 US-09-864-761-14164	US-09-880-457-1 US-09-880-457-3 US-09-880-457-2 US-09-877-650-12 US-09-871-856-12 US-10-017-910-1	ID
Sequence 1690, Appl Sequence 96, Appli Sequence 3, Appli	4	Sequence 10, Appl Sequence 10, Appl Sequence 3, Appli Sequence 9, Appli Sequence 14164, A	Sequence 1, Appli Sequence 3, Appli Sequence 2, Appli Sequence 12, Appli Sequence 12, Appli Sequence 1, Appli	Description

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27.8 27.6 27.6	27.8 27.8 27.8	28.2 28.2 28.2 28.2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	30.2 30.2 29.6 29.4 29.4 28.8
				11.6 11.5 11.3 11.3 11.3 11.0
465237 371 486 608	932 666 2147 2222	477 477 477 2000 398	357 407 1365 1365 477 477	2000 30 2048 409 2244 257 143068
10		10	10 10 10	10 10 10 10
US-09-933-207A-1 US-09-834-975-285 US-09-783-590-10438 US-09-759-143-193	US-09-925-300-515 US-09-764-864-590 US-09-981-353-104 US-09-981-353-76	US-09-938-965-5848	US-09-878-574-3028 US-09-878-574-3146 US-09-815-242-4243 US-09-815-242-8196 US-09-759-143-92 US-09-759-143-92	US-09-887-576-151 US-09-880-457-8 US-09-764-847-1468 US-09-783-590-1953 US-09-764-864-153 US-09-876-754-768
Sequence 10438, App Sequence 10438, A Sequence 193, App	Sequence 515, App Sequence 590, App Sequence 104, App Sequence 76, Appl Sequence 1, Appli	Sequence 92, Appl Sequence 92, Appl Sequence 4251, Ap Sequence 5848, Ap	Sequence 3028, Applesquence 3146, Ap Sequence 4243, Ap Sequence 8196, Ap Sequence 92, Appl Sequence 92, Appl Sequence 92, Appl Sequence 92, Appl	Sequence 151, App Sequence 8, Appli Sequence 1468, Ap Sequence 1953, Ap Sequence 7063, Ap Sequence 7063, App Sequence 316, App

ALIGNMENTS

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NUMBER OF SEQ ID NOS: 9

SEQ ID NO 1

LENGTH: 1161

TYPE: DNA

ORGANISM: Homo sapiens
US-09-880-457-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/09880457; Patent No. US20020106728A1; GENERAL INFORMATION:
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APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
FILE REFERENCE: P2871R1
                                                                                                                                                                                                                                                                                                                          Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                          666 ATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTATGG 725
                  181 ATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTATGG 240
                                                                                                                                                                                                                                                                                                                        y Match 100.0%; Score 261; DB 10; Local Similarity 100.0%; Pred. No. 1.6e-77;
                                                                                                                                                                                    61 GAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
                                                                                                                                                                                                                                                                                                          0; Mismatches
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241 TGTAATTTGAGAATCATTCAC 261

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US-09-880-4<u>5</u>7-2
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US-09-880-457-2
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TYPE: DNA

ORGANISM: Homo sapiens

US-09-880-457-3
                 SEQ ID NO 2
LENGTH: 2412
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-880-457-3
                                                                                                                           APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
CURRENT APPLICATION UNMBER: US/09/880,457
CURRENT APPLICATION UNMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
CURRENT FILING DATE: 2001-06-12
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09880457
Patent No. US20020106728A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 3
LENGTH: 1186
                                                                                          PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 251; Conservative
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.

TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
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RESULT 4
US-09-877-650-12
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                                                                                                              TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
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APPLICATION NUMBER: 08/995,659

FILING DATE: 1997-12-22

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 2852-A TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Anderson, Dirk M.
                             LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                 TOPOLOGY: linear
                                                                                                                                                                                                       NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693
                                                                                                                                                    TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/877,650 FILING DATE: 08-Jun-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: WA
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US-09-877-650-12
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US-09-871-856-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 593 ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG 652
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                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
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Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
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LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                                           STATE: WA
                                                                                                                 APPLICATION NUMBER: 08/996,139 FILING DATE: <Unknown>
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74.88;
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Sequence 1, Application US/10017910
Patent No. US20020159970A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 ACATGACTITCAGCAACGGAAAACTAAGAGTCA----AAGGCATTTATTACCGGAATG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    653 CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             593 ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 46.48;
Local Similarity 74.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
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TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: cDNA HYPOTHETICAL: NO
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                           NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: Klauber & Jackson
                                                                                                                                                                                                                      TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
                                                                                                                                                                                                                                                                                                               APPLICANT: Choi, Yongwon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 954 base pairs TYPE: nucleic acid STRANDEDNESS: single
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE: huRANKL (full length)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: <Unknown>
                                                                                                                            STREET: 411 Hackensack Avenue, 4th Floor
                                                                        COUNTRY: USA
                                                                                            STATE: New Jersey
                                                                                                              CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                              Steinman,
                                                                                                                                                                                                                                                                                                 Wong, Brian
                                                                                                                                                                                                                                                                              Josien, Regis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .951
                                                                                                                                                                                                         METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                Ralph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 121.2; DB . Pred. No. 7.2e-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8;
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Sequence 10, Application US/09877650 Patent No. US20020169117A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTGGGGTAAGATCTCCA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 GCT--CATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCCATGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 45.2%; Score 118; DB 9; Length 1823; Local Similarity 74.0%; Pred. No. 1.1e-29; Length 1823; Mismatches 55; Indels
                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
                                                                                                                                    Gailbert, Laurent
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                               APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1823 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/447,035
ETLING DATE: 1999-11-22
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 14-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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                                 STATE: WA
                                                       CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
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TELEFAX: 201-343-1684
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SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                Galibert,
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; Sequence 10, Application US/09871856
                            US-09-871-856-10
                                                RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                645 CT 646
                                                                                                                                                      235 CT 236
                                                                                                                                                                            585 GCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG 644
                                                                                                                                                                                                    175 GCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAG 234
                                                                                                                                                                                                                                                              525 AACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC
                                                                                                                                                                                                                                                                                    121 AACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAAT 174
                                                                                                                                                                                                                                                                                                                                           465 GGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCT 524
                                                                                                                                                                                                                                                                                                                                                                                                                             63 GG--CTCATAAAAACGAGTCTTTCTTTCGAAAACATGACCAAGATTGGGCAAAACGTCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCCATCAATATCCCCATGA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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LOCATION: 3...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: RANKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1630 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/995,659 FILING DATE: 1997-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.6%; Score 95.6; DB 9; Length 1630; 68.2%; Pred. No. 3.2e-22; tive 0; Mismatches 69; Indels 8
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US-10-017-910-1

FEATURE

Query Match Matches

RESULT 7 US-09-877-650-10 ; Sequence 10, Ap

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Best Local Similarity
                                                                                                                                                                                                                                         Matches 165;
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        525
                                    121 AACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAAT 174
                                                                                    465
                                                                                                                                                                405
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FILING DATE: CUNKDOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
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COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
AACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC 584
                                                                                                                                                                                        GGCAATCCTGACGCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGA 62
                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, Dirk M
                                                                                                                  GG--CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
                                                                                                                                                       GGCAAGCCTGAGGCCCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCG 464
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                                                                             GGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCT 524
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 3...
                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: RANKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/871,856 FILING DATE: 31-May-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                         Conservative
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68.2%;
                                                                                                                                                                                                                                                                                                                                                          .884
                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                      Score 95.6; DB 10
Pred. No. 3.2e-22;
                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                     69;
                                                                                                                                                                                                                                                                          Length 1630;
                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                     Gaps
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NAME/KEY: CDS;
; LOCATION: 142..1092;
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-017-910-3
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US-10-017-910-3
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Patent Mo. US/2002019970A1
GENERAL INFORMATION:
APPLICANT: Choi, Yongwon
                                                                                   Matches
                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
610 GGCAAGCCTGAGGCCCAGCCATTTGCACCACCTCACCATCAATGCTGCCAGCATCCCATCG 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          645 CT 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 GCCGACATTTGCTCTGGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAG 234
                                                                                                      Local
                           3 GGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTAATAACCATCAATATCCCATGA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/017,910
FILING DATE: 14-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/447,035
FILING DATE: 1999-11-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steinman, Ralph
TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                   165;
                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 600-1-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Esq., David REGISTRATION NUMBER: 26,74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 411 Hackensack Avenue, 4th Floor CITY: Hackensack
                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2237 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Klauber & Jackson
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choi, Yongwon
Wong, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Josien, Regis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
                                                                                                36.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHODS OF USE THEREOF
                                                                               Score 95.6; DB 9;
Pred. No. 3.7e-22;
0; Mismatches 69;
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                                                                                                                   Length 2237;
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                                                                               8
                                                                             Gaps
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FILING DATE: 2000-08-03

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; Sequence 14164, Application US/09864761

; Patent No. US20020048763A1
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US-09-880-457-9
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LENGTH: 61
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Best Local Similarity
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                                                                                                                                          APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-66-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILTING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                              APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                       CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                       David R.
, David K.
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100.0%;
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. 2.7e-11;
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RESULT 12
US-10-040-739-93
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                                                                                                                                            Sequence 93, Application US/10040739 Patent No. US20020173635A1 GENERAL INFORMATION:
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SEQ ID NO 14164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 454
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                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
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NUMBER OF
                                                                                                                                                                                                                                                                  TCTGTAAATAAAATACGGCATTATCTAGCAAAATTACGTA
                                                                                                                                                                                                                                                                                                 TTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTA 201
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                                                                                                                                                                                                                                                                                                                                                                                                    81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
          Merberg, David
Treacy, Maurice
Spaulding, Vikki
OF INVENTION: SECRETED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
SEQUENCES:
                                                                                                                              Jacobs, Kenneth
                                                                                               McCoy, John
LaVallie, E
                                                                               Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
               EXPRESSED SEQUENCE TAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 454;
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CORRESPONDENCE ADDRESS:

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APPLICANT: King, Gordon E.

APPLICANT: Meagher, Madeleine Joy

APPLICANT: Xu, Jiangchun

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.547

CURRENT APPLICATION NUMBER: US/09/920,300A

CURRENT FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 1789

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1691

LENGTH: 985

TYPE: DNA

ORGANISM: Homo sapiens
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                                                                                         US-09-920-300A-1691
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US-09-920-300A-1691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: 93: US-10-040-739-93
        Matches
                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1691, Application US/09920300A Patent No. US20020136728A1
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 CTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,739
FILING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 ATTGAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATGGGCAGAAATT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 AAACAACGAGCCAAGCTCCAGAAAATGTTGCCCAAGCTGGAAGAAGAGTTGAAGGCACGA 376
                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 ATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGA 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/036,520 FILING DATE: 03-JUN-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linea
MOLECULE TYPE: cDNA
        63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 493 base pairs TYPE: nucleic acid STRANDEDNESS: double
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    Mismatches
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    53;
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Gaps
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APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: U$/10/033,528
CURRENT APPLICATION NUMBER: U$/12-26
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1691
SEQ ID NO 1691
LENGTH: 985
TYPE: DNA
ORGANISM: Homo sapiens
US-10-033-528-1691
                                              Qy
                                                                                                                                                                               ; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10910
; LENGTH: 3073
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-701-10910
    DЬ
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APPLICANT: King, Go.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                             Matches
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10910, Application US/09867701 Patent No. US20020132237A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1691, Application US/10033528 Patent No. US20020131971A1
                                                                                                                                                                                                                                                                                                           APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
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1270 AAACAACGAGCCAAGCTCCAGAAAATGCTGCCCAAGCTGGAAGAAGAGTTGAAGGCACGA 1329
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                       68 ATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGA 127
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Local Similarity 54.3%;
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Local Similarity 54.3%;
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Meagher, Madeleine Joy
                                                                                           Conservative
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Search completed: December 8, 2002, 19:37:57 Job time: 24.2491 secs

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Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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**Cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

**Cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

**Cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

**Cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

**Cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

**Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

**Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

**Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

**Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

**Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

**Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

1. Cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

1. Cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

2. Cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

3. Cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

4. Cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
  10 US-09-880-457-1
10 US-09-880-457-2
10 US-09-80-457-3
9 US-09-877-650-12
10 US-09-877-650-10
10 US-09-877-650-10
10 US-09-877-650-10
10 US-09-871-856-10
10 US-09-871-856-10
10 US-09-880-457-9
10 US-09-880-457-9
10 US-09-887-701-6187
10 US-09-867-701-1068
10 US-09-867-701-1068
10 US-09-18-686-9
10 US-09-918-686-9
10 US-09-918-686-9
10 US-09-918-686-1
  9 US-10-17-910-3

10 US-09-880-457-9

10 US-09-835-232-6

10 US-09-827-246-3

10 US-09-867-701-10680

10 US-09-867-701-10680

10 US-09-764-869-1690

10 US-09-918-686-2

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                    Sequence 3, Appli
Sequence 6187, Ap
Sequence 10680, A
Sequence 1690, Ap
Sequence 2, Appli
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Sequence 1, Appli
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sequence 12, Appl
                                                                                                                                                                                                                                                          Sequence 3,
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sequence 10, Appl
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1	Sequence 442, APP	Sequence 3930, AP	Sequence 529, APP	1 1	292	469	Sequence 440, APP	Sequence 393, APP		7 4 0	2	245,		ب	Sequence 3, APPLI	3/4//	2727		Sequence 15062, A	4893,		Sequence 646, APP	Ĺ	7	۱ د	1005		Seguence 14364, A	۲,	Sequence 3, Appli

ALIGNMENTS

US-09-880-457-1

Sequence 1, Application US/09880457 Patent No. US20020106728A1

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; TYPE: DNA; ORGANISM: Homo sapiens US-09-880-457-1
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APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
APPLICANT: TITLE OF INVENTION: for the Treatment of Body Weight Disorders
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
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LENGTH: 1161
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CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-66-12
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/212,901 PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
121 AAGGACGTGGTTGCGAGGACATGGAGGGAAAGTTCTACAGAGGAGGACACTGGGCTTCA 180
121 AAGGACGTGGTTGCGAGGACATGGAGGGAAAGTTCTACAGAGGAGGCACAGTGGGCTTCA 180
                                                                                                                                   Mismatches
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                       Sequence 2, Application US/09880457
Patent No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
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APPLICANT: Goddard, Audrey APPLICANT: Wood, William I.
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                                                                                                                                                                                                                                      CCACAGGACAAAGCATGATGTGTATGTCCTCACTAAATGGCAATGTCCTTGAGAAGAC 1080
                                                                                                                                                                                                                                                                         GGATTTGCATTTGTGGATGAACTTGTGTGTTCAGCTGAAGGCTGAAGTTGTAACTCTGAA 1020
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SEQ ID NO 2
LENGTH: 2412
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                         1935 TCAAAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 1994
                                                                                                                           1875 AACATGACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAG
                                                                                                                                                                                        TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use TITLE OF INVENTION: for the Treatment of Body Weight Disorders FILE REFERENCE: P2871R1 CURRENT APPLICATION NUMBER: US/09/880,457 CURRENT FILING DATE: 2001-06-12 PRIOR APPLICATION NUMBER: US 60/212,901 PRIOR FILING DATE: 2000-06-20
                   697 GCCTAACTCTGCAGGACCTTCAGCTATGGTGTAATTTGAG 736
                                                                                                                                                                                                                                                       1755 TAATAGGGAGAAAGAAGTATTTGCTAAGAATGGCAATCCTGATGCTCAGCCTTCAACTCA 1814
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                                                                          637 TCAAAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                                                                          577 AACATGACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAG
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GCCTAACTCTGCAGGACCTTCAGCTATGGTGTAATTTGAG 2034
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LENGTH: 1186
TYPE: DNA
ORGANISM: Homo sapiens
US-09-880-457-3
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US-09-877-650-12
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Patent No. US20020106728A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/09877650 Patent No. US20020169117A1 GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
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                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGC 669
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               PRIOR
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                             APPLICATION NUMBER: US/09/877,650 FILING DATE: 08-Jun-2001 CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                               CITY: Seattle
                                                                                                                                                                                                                                                                               ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                   ZIP: 98101
                                                                                                                                                                                                                                           STATE: WA
APPLICATION NUMBER: 08/995,659
                                                                                                                                                                                                                           COUNTRY: USA
                 APPLICATION DATA:
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100.0%; Pred. No. 3.1e-76;
ative 0; Mismatches 0;
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US-09-877-650-12
                                                                                                                                                                                                                                 Sequence 12, Application US/09871856; Patent No. US20020081720A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCGGAAACATG 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              629 AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       640 ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        509 TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG 568
                                                                                                                                                                                                                                                                                                                                                                                           689 ACCTAGCTACAGAGTATCTTCAACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                  697 GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 10.9%;
Local Similarity 72.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                  TITLE OF INVENTION: Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 954 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 2852-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Perkins, Patricia Anne
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: huRANKL (full length)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY:
                                                           ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                       STATE: WA
                                           CITY: Seattle
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE:
                                                                                                                                                                     Galibert, Laurent
Maraskovsky, Eugene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 126; DB 9; Length 954; Pred. No. 2.2e-30;
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; Sequence 1, Application US/10017910
; Patent No. US20020159970A1
                                             RESULT 6
US-10-017-910-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEBHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                    689
                                                                                                                                                                    697 GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                            640 ---AAGGCATTTACTGCAGAATGCCGAGATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                                                                                                                                                                                                         569 ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC 628
                                                                                                                                                                                                                                                                                                                  583 ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACCTAAGAGTCA--- 639
                                                                                                                                                                                                                                                                                                                                                                            509 TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG 568
                                                                                                                                                                                                                                                                                                                                                                                                                   525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                        AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG 688
                                                                                                                           ACCTAGCTACAGAGTATCTTCAACTA 714
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FILING DATE: <UNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT_INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: huRANKL (full length)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 126; DB 10;
Pred. No. 2.2e-30;
0; Mismatches 65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1823 base pairs
                               413 AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG 472
697 GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                      640 ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                             353 ATCGGGGGTGGGGTAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC 412
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                                                                                                                                                   583 ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA--- 639
                                                                                                                                                                                                                 525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTCTTGGAAACATG 582
                                                                                                                                                                                          293 TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG
                                                                                                                                                                                                                                                                       233 CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 292
                                                                                                                                                                                                                                                                                                          465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 09/447,035 FILING DATE: 1999-11-22 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Choi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/017,910 FILING DATE: 14-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 133521
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                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                        10.6%; Score 122.8; DB 9 71.8%; Pred. No. 3.6e-29;
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                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           DB 9;
                                                                                                                                                                                                                                                                                                                                                        67;
                                                                                                                                                                                                                                                                                                                                                                                           Length 1823;
                                                                                                                                                                                                                                                                                                                                                        Indels
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US-09-877-650-10
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                                                                                                                                                                                                  US-09-877-650-10
                                                                                                                      Matches
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473 ACCTAGCTACAGAGTATCTTCAACTA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                            477 TIGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCA 536
537 ATATCCCATGAGG--CTCATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGG 594
                                      394 TGGCCCAGCGAGGCAAGCCTGAGGCCCAGCCATTTGCACACCTCACCATCAATGCTGCCA 453
                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anderson, Dirk M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 2852-A TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                      170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/877,650 FILING DATE: 08-Jun-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                        SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                    CLONE: RANKL
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                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 3..8
                                                                                                                                                                                                                                                                                                                         LIBRARY: <Unknown>
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1630 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (206)233-0644
                                                                                                                                       8.4%;
67.2%;
                                                                                                                                                                                                                                             .884
                                                                                                                      Score 97; DB 9; Length 1630; Pred. No. 7.3e-21; 0; Mismatches 75; Indels
                                                                                                                                 8; Gaps
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                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
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TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 98101
COMPUTER READABLE FORM:
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NAME: Perkins, Patrici
                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                           FEATURE:
                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             ANTI-SENSE: NO
                                                                                                                                                                                                  HYPOTHETICAL: NO
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                         ORGANISM: Mus musculus
                                                                                                                                                                                                                                                          STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                LENGTH: 1630 base pairs
                       LOCATION:
                                                                                CLONE: RANKL
                                                                                                   LIBRARY:
                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galibert, Laurent
                                                                                                 <Unknown>
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US-10-017-910-3
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                                                            INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 67.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     649 ATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGC 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   477 TIGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTAATAACAATCA 536
                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/017,910 FILING DATE: 14-Dec-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAMETHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Choi, Yongwon
Wong, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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STRANDEDNESS: double
                     TYPE: nucleic acid
                                                                                                                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
                                         LENGTH: 2237 base pairs
                                                                                                                         TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                          TELEX: 133521
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 09/447,035 FILING DATE: 1999-11-22
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Hackensack
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Pred. No. 7.3e-21;
0; Mismatches 75; Indels
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SEQ ID NO 9

LENGTH: 61

TYPE: DNA

ORGANISM: Artificial Sequence
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                                                                                                                                                                                           Matches
                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pan, James
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                                                               677 A 677
                                                                                                            617 CAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATTGCCGGCACATTTGCTCTCG 676
                       61 A 61
                                                                                       1 CAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATTTGCTCTCG
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                                                                                                                                                                           Match 5.3%; Score 61; DB 10; Local Similarity 100.0%; Pred. No. 3.6e-10; es 61; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.4%;
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Pred. No. 9.1e-21;
0; Mismatches 75; Indels
                                                                                                                                                                                                                   Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2237;
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US-09-835-232-6/c
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NAME/KEY: misc_feature

LOCATION: (1)...(180216)

OTHER INFORMATION: n = A,T,C or G

US-09-835-232-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 6, Application US/09835232
Patent No. US20020098489Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 124718 AAGCACCTACTAAGTACCAGGCACTATTTGGGATGTGGGGGACACAACAAGAGGAAAAACT 124659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 124598 AGGCAACCAAATGC 124585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-822-246-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Leder, Philip
APPLICANT: Leder, Benjamin
APPLICANT: Leader, Benjamin
TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 00383/052002
FILE REFERENCE: 00383/052002
CURRENT APPLICATION NUMBER: US/09/835,232
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 60/196,811
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 6
LENGTH: 180216
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09822246

Patent NO. US20020142383A1

GENERAL INFORMATION:
APPLICANT: MERKULOV, Gennady et al.
APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                  US-09-822-246-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 197997
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                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/822,246
CURRENT FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 4
                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 AAGTATCTACAAGGCACCAGGCATTTTTGAGCATTTGGGGATTTGTCAGCAAACAAGTCA 406
                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)...(197997)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                     ORGANISM: Human FEATURE:
                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             467 GGAGAAGTATTTGC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 3.3%; Score 38; DB 10; Length 180216; Local Similarity 55.2%; Pred. No. 2; es 74; Conservative 0; Mismatches 60; Indels 0;
                363 CCAGGCATTTTTGAGCATTTGGGATTTGTCAGCAAACAAGTCAGACAAAAAACCTTGCT 422
                                                                                Local
h 3.3%; Score 38; DB 10; Length 197997; Similarity 65.1%; Pred. No. 2.1; 56; Conservative 0; Mismatches 30; Indels 0;
       30; Indels 0;
              0; Gaps
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Db 180595 TTGATAGAGCTTATATTCTATAATAG 180620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 6187, Application US/09867701 patent No. US20020132237A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6187
LENGTH: 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Aglate, Paul A.
APPLICANT: Aglate, Robert
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICATION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
NUMBER OF SEQ ID NOS: 10912
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NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10680, Application US/09867701 Patent No. US20020132237Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: A07
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                  LENGTH: 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  715 TTCAGCTATGGTGTAATTTGAGAATCATTCACTGAGCATCAACTATGTAACCAGCATTGG 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             775 GTTGGGTGCCAGAGATCCAAAGCTAAGACA 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 3.1%;
Local Similarity 62.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 TTCGTTCATTTATTCATTCAACAAACATTATATGAGCACCCACTATGTGCCAGGCACAGT 64
                                                                                                                         715 TTCAGCTATGGTGTAATTTGAGAATCATTCACTGAGCATCAACTATGTAACCAGCATTGG 774
                                         775 GTTGGGTGCCAGAGATCCAAAGCTAAGACA 804
  65 GTTAGGTCCCACACATACAGAGCTGAATCA 94
                                                                                                                                                                                           Local
                                                                                  5 TICGTICATITATICATICAACAAACATTATATGAGCACCCACTATGTGCCAGGCACAGT 64
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                                                                                                                                                                           56;
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Similarity 62.2%;
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                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35.6; DB 10; Length 370; pred. No. 0.19;
                                                                                                                                                                             score 35.6; DB 10; Length 495; pred. No. 0.24; 0; Mismatches 34; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34; Indels
                                                                                                                                                                                             0; Gaps
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0;

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RESULT 15

US-09-764-869-1690/c

Sequence 1690, Application US/09764869

Retent No. US20020061521A1

REPERENT ELICENTION WILLEL ACIDS, Proteins, and Antibodies

FILE REPERENCE: PC007-

CURRENT FILED ON INVERT: US/09/764,869

PITO: APPLICATION NUMBER: US/09/764,869

PITO: APPLICATION ON UNBER: US/09/764,869

PITO: APPLICATION
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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373
1 HEAHKTSLSSWKHDQDWANV.......TSAGLTLQDLQLWCNLRIIH 68
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                                                                                                                                                                                                                                                                                                                                                                                            671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
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                                                                                                              sp_phage:*
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sp_archeap:*
           sp_bacteriap:*
                          sp_rvirus:*
                                      sp_vertebrate:*
sp_unclassified:*
                                                                    sp_virus:*
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sp_human:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

11 10 10 11 11 11 11 11 11 11 11 11 11 1	Result No.
64.5 63.5 62.6 63.5	Score
18.5 18.5 18.0 18.0 18.0 17.3 17.3 17.3 17.3 17.3 17.3 17.3 17.3	% Query Match Length
214 1130 187 296 307 478 276 1000 1018 1090 1214 297 287 287 281 287	Length I
13 15 10 110 110 110 110 110 110 110 110 1	DB
09bDz5 Q88282 Q88282 Q9FGA8 Q9FT467 Q9FT46 Q9T146 Q9T146 Q9T189 Q9UIB9	SUMMARIES ID
Q9ddz5 brachydanio Q88282 snakehead r Q88282 snakehead r Q9fg38 arabidopsis cys297 thermotoga Q9ff49 arabidopsis Q71146 human inmun Q91146 homo sapien Q960350 homo sapien Q960350 homo sapien Q960350 homo sapien Q9750 drosophila Q913x9 pseudomonas Q90750 pseudomonas Q90750 sapien Q9750 sapie	Description

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15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.5	15.5	15.5	15.7	15.7	15.7	15.7	15.8	15.8	16.0	16.0	16.0	16.0	16.0	16.1	16.1	16.1	16.1	16.4	16.4	16.4	16.4
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Q9VUN0	Q9NBK9	Q99LF9	Q92IP3	Q99YE2	Q9JRL2	Q9FAC1	081015	058765	08R5Y5	097B.T7	096BW9	09X6N2	022506	Q8RFS0	068768	Q9K9G9	Q92NK4	Q8XDI7	Q82K87	097516	O8XTZ4	0989R7	Q8UDK4	Q8YZI4	O8RHH7	045818	09VFV1	095xD5
Q9vun0 drosophila	04440000 P111	אפררפו	092in3 ricko++cic	Shoot at the cococococococococococococococococococo	091712 1317 CE	Ogfac1 streetonico	OBIOIS Priococcus		Q9/DJ/ Chermoplasm			aenor nabo		yersinia p	OS87SS WORTHING III	INTERCETIFIED			O87k87 salmonolla		MITGOZIUI	ayrobacter	OBUNIA TOTAL SP	Tusopacte	caenor nabgi			, 1

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Q9DDZ5
                                                                             Matches
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Best Local :
                                                                                                                                PROSITE; PS50049; TNF_2; 1.
SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;
                                                                                                                                                                    ProDom; PD002012; TNF_abc; 1. SMART; SM00207; TNF; 1.
                                                                                                                                                                                                   ZFIN; ZDB-GENE-010801-1; tnfsf101.
InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                     "Molecular cloning and expression of a TNF receptor and two TNF ligands in the fish ovary.", Comp. Biochem. Physiol. B, Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001). EMBL; AF250041; AAG47640.1; -... HSSP; P50591; 1D0G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9DDZ5 PRELIMINARY; PRT; 214 AA.
Q9DDZ5;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                      Bobe J., Goetz F.W.;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNFSF10L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRAIL-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7955;
76 HOSCRHPVHTWANKSFGAHLYNMTLTNGRLRVPODGRYYLYSQVYFRY 123
                   1 HEAHKTSLSSWKHDQDWANVSNMTFSNGKLRV--KGIYYRNADICSRH 46
                                                                               Match 18.5%; Score 69; DB 13; Length 214; Local Similarity 31.2%; Pred. No. 1.2;
                                                                            15;
                                                                          Conservative
                                                                   13; Mismatches
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                                                                 2;
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RESULT 2

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Best Local
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Best Local
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Q88282; PRELIMINARY; PRT:
Q88282;
Q1-NOV-1996 (TrEMBLrel O1, Last seq
Q1-NOV-1996 (TrEMBLrel 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=96211493; PubMed=8648695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sanotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
similarity to pollen-specific protein Bnml.
Arabidopsis thallana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Evidence for a new retrovirus genus of piscine origin." submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9FGA8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hart D., Frerichs G.N., Rambaut A., Ronalds R.J., Onions D.E.; "Evidence for a new retrovirus genus of piscine origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete nucleotide sequence and transcriptional analysis snakehead fish retrovirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hart D., Frerichs G.N., Rambaut A.,
                                                                                                                                                                                                                                                                                                                "Structural analysis of Arabidopsis thaliana chromosome 5. Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AB026650; BAB10289.1; - SEQUENCE 187 AA; 20056 MW; 305781D3A0738AEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Katoh T., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              476 SSGNSWKAEIDKIRKQKW----QKCYFSGKLRIKGTDYEEIDTCPKPLIGPLSGFIPTGV 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532 TKTLKTGVTWTTAVVKIDLQQWVDI 556
                                                                  102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virol. 70:3606-3616(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 TSLSSWKHD-----QDWANVSNMTFSNGKLRVKGIYYRNADICSRHRV-----TSA 51
   54 TLQDLQL 60
                                                                                                                          1 HEAH-----KTSLSSWKHDQDWANVSNMTFSNGKLRVKGTYYRNADICSRHRVTSAGL 53
                                                              HDAYVGILASLKSALLELKDSPDTANYDVMVSGDDTRRVKGLVEKNTDTASK----TLMEM 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retroid viruses; Retroviridae; Epsilonretrovirus
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128317 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asamizu E., Sato S., Nakamura Y., Kotani H.,
                                                                                                                                                                                                                             18.2%; Score 68; DB 32.8%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 69; DB Pred. No. 8.7;
                                                                                                                                                                                                      9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B6A4F8095E4F0D3F CRC64;
                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1130 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 15;
                                                                                                                                                                                                                                                              DB 10; Length 187;
                                                                                                                                                                                                         26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1130;
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Q9FT49
                                                                                                                                                        A CONTRACTOR OF THE CONTRACTOR
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                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9FT49
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                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9X2G7

O9X2G7;

O1-NOV-1999 (TrEMBLrel. 12,

O1-NOV-1999 (TrEMBLrel. 20,

O1-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein TM1852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR, TM1852; ...
Hypothetical protein; Complete proteome.
SEQUENCE 296 AA; 34197 MW; 11B3980CA5C3D2C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-MSB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2336;
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                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Eukaryota; Viridiplantae; Streptophyta; core e
spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
                                                                                                                                    EU Arabidopsis sequencing project; submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL132972; CAC07924.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical 34.9 kDa protein.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Alcaraz J.P., Clabault G., Cottet A., Mache R., Mewes H.W.,
Lemcke K., Mayer K.F.X., Quetter F., Salanoubat M.;
                                                                                                                                                                                                                                                         Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                     eurosids II;
                                                                                                                       Hypothetical protein
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      r25B15_100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 EEDWEKFGGVPNVVFSDAMIEYNGYYYVYYGAADNC----IALATIPVEKVMKWC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 DQDW---ANVSNMTFSNGKLRVKG---IYYRNADICSRHRVTSAGLTLQDLQLWC 62
Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE001822; AAD36914.1; ~.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / DSM 3109;
                                                                                                   307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
  Conservative
                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.0%; Score 67; DB: 27.3%; Pred. No. 3.1; tive 11; Mismatches
                                                                                                   34863 MW;
                           18.0%;
18.3%;
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         19;
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                             Score 67; L
Pred. No: 3.
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                                                                                                   DC8746CB47D8F92E CRC64;
            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Embryophyta;
                                                         DB 10;
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            26;
                                                                                                                                                                                                                                                                                                                                                                                                                                       core eudicots; Rosidae;
                                                      Length 307;
            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tracheophyta;
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                 22;
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RESULT 6
Q71146
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OCC GER BRADA
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Best Local S
                                                                                                                                                                                                                                                                                                                                           Matches
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 HDEYKYLSETWRHNKEWKYRSEHHYLYLGARTSWKKTQCHIHHLPYSOG-ITINGYLYYG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Envelope glycoprotein gpl20 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 AWIDDKCVLMSFDLTSEDVGVW 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quinones-Mateu M.E., Dopazo J., Este J.A., Rota T.R., Domingo E., "Molecular characterization of human immunodeficiency virus type 1 isolates from Venezuela.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96093896; PubMed=7576917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 ADICSRHRVTSAGLTLQDLQLW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quinones-Mateu M.E., Holguin A., Dopazo J., Najera I., Domingo E.; "Point mutant frequencies in the pol gene of human immunodeficiency virus type 1 are two- to threefold lower than those of env."; virus type 1 are two-touriuses 12:1117-1128(1996).

AIDS Res. Hum. Retroviruses 12:1117-1128(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIDS Res. Hum. Retrovituses :
EMBL; U16766; AAC55683.1; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               AIDS;
                                                     01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Possible glucanotransferase (putative endo alpha-1,4
polygalactosaminidase related protein).
CACO736.
            Bacteria; Firmicutes; Bacillus/Clostridium Clostridiales; Clostridiaceae; Clostridium
                                        Clostridium acetobutylicum
 NCBI_TaxID=1488;
                                                                                                                                                                                                                                                      44 SRHRVTSAGLTLQDLQLWCNLRII 67
                                                                                                                                                                                                                                                                                  74 OMHEDIISLW--DOSLKPCVKLTPLCVTLDCTDWGNATNTNISSGGAMERG----EIKNC 127
                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 21; Conserv
                                                                                                                                                                                                                                                                                                               2 EAHKTSLSSWKHDQ------DWANVSNMTFSNGKLRVKGIYYRNADIC 43
                                                                                                                                                                                                                               SENITTSSGEKMOKEALFYNLDVV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                            Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                        478 AA;
                                                                                                                                                                                                                                                                                                                                           18.0%; Score 67; DB i
illarity 25.0%; Pred. No. 5.5;
Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       478
                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                        53554 MW; 103F636765B51D92 CRC64;
                                Bacillus/Clostridium group; Clostridia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 AA.
                                                                                                                                                                       276 AA.
                                                                                                                                                                                                                                                                                                                                                                                  DB 15; Length 478;
                                                                                                                                                                                                                                                                                                                                                          27; Indels
                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 8
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                                                                                                                                    RESULT 9
                                                                                                                                                                                                    g
OC GN DT DT AC OC OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed=11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838(2001).
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                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9UIB9:

01-MAY-2000 (TrEMBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     о901В9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 NWK-DESWIDVSNLKWDNYVVNTLGKNLKNKGVDGFFLDNLDVYSKYKKDSMFIGLLNI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Romero M.F.; Romero M.F.; with the National contraction of a HCO3 transporter, NT2-NBC, from human brain, similar to both the Anion exchangers (AEs) and the Na/Bicarbonate Cotransporters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bicarbonate transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 SWKHDQDWANVSNMTFSN-----GK-LRVKGI---YYRNADICSRHRVTSAGLTLQDL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF053755; AAF21720.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00955; HC03_cotransp; 1. PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                       HSSP; p02730; IBNX:
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotransp.
                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                TIGREAMS; TIGRO0834; ae;
SEOUENCE 1000 AA; 112
                                          01-AUG-1998 (TIEMBLrel. 07, Created)
01-AUG-1998 (TIEMBLrel. 07, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
sodium bicarbonate cotransporter2.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                         060350
                                                                                                                                                                                                    564 TLAQWKKDNITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GPYIPDVLFWC 614
                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                               7 SLSSWKHDQDWA-NVS--NWTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQDLQLWC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Conservative
                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e; Complete proteome.
276 AA; 32104 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.3%; Score 64.5; Di
30.5%; Pred. No. 5.9;
                                                                                                                                                                                                                                                                      17.3%; Score 64.5; D
32.2%; Pred. No. 28;
tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                   112501 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                       93FAA40A3141F8F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1000 AA
                                                                                                                                        1018 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 276;
                                                                                                                                                                                                                                                                                                          DB 4; Length 1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Indels
                                                                                                                                                                                                                                                                                  17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                       11;
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Q9Y6M7
                                                                                                                     RESULT 11
09Y6M7 PRELIMING...,
09Y6M7; PRELIMING...,
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                654 TLAQWKKDNITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GPYIPDVLFWC 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                    PRINTS; FRANCE 1090 AA; 123080 MW; 541839CC9B565896 CRC64;
                                                                                                                                                                                                                                                               InterPro: IPR003020; HCO3_cotransp. Pfam; PF00955; HCO3_cotransp; 1.PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                 Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF089726; AAG16773.1; -. HSSP; P02730; 1BNX.
                                                                                                                                                                                                                                                                                                   InterPro; IPR001717; Anion_exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09HC88;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Sodium bicarbonate cotransporter 2b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                             FISSUE=KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                         7 SLSSWKHDQDWA-NVS--NMTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQDLQLWC 62
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens sodium bicarbonate cotransporter 2b mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     оэнсва
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          564 TLAQWKKDNITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GPYIPDVLFWC 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotransp.
Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commu
EMBL; AB012130; BAA25898.1;
HSSP; P02730; IBNX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ishbashi K., Sasaki S., Marumo F.;
"Molecular cloning of a new sodium bicarbonate cotransporter cDNA from human retina.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-RETINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 SLSSWKHDQDWA-NVS--NWTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQDLQLWC 62
                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocal Similarity
                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                   Abuladze N., Newman D., Hwang J., Kurtz I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR00834; ae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1018 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                    17.3%; Score 64.5; 32.2%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.3%; Score 64.5; DB 4; I
32.2%; Pred. No. 28;
ative 12; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114204 MW; A37799D93A1E30BC CRC64;
                                                                                                                                                                                               12;
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                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                        _ DB 4; Length 1090;
                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.
                                                                                                                                                                                  17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 1018;
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RX MEDLINE=SURINGLEL;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Buril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Godek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey M., Helman T.J., Wei M.-Harris M.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9VCJ9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JIN-2002 (TrEMBLrel. 21, Last annotation update)
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EMBL; AF047033; AAD38322.1; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotransp.
Pfam; PF00955; HCO3_cotransp; 1
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 SLSSWKHDQDWA-NVS--NMTESNGKLRVKGIYYRNADICSRHRVTSAGLTLQDLQLWC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSUE=SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.3%; Score 64.5; 32.2%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136042 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EF203500B5BF5267 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 1214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 functional
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RESULT 13
Q9I3X9
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RRA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RRA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RRA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RRA Spler E., Spradling A.C., Stagleton M., Strong R., Sun E.,
RRA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RRA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RRA Walliams S.M., Woodsge T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RRA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RRA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
"The genome sequence of Drossphila melanogaster.";
RT "The genome sequence of Drossphila melanogaster.";
RT Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                      Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V., "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
Receptor; Complete proteome.
SEQUENCE 813 AA; 89127 MW;
                                                                   opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004565; AAG04754.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00089; trypsin; 1.

PRINTS; PR007722; CHYMOTRKPSIN.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.

PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                            STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
                                                                                                                                                                                                                                                                                                                                                                                                    Probable siderophore receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rlyBase; FBgn0039101; CG16710.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000169; SHprot_acsite.
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                        Pseudomonas
                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE003744; AAF56159.1; -. HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 HKLQIAGWGLSHKQGYSNVLLQAYVNG-----RNADECS
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15; Conser
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297 AA; 33480 N
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34.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Last
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Pred. No. 8.6;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation
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 3E61AB56E3105299 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
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RESCUTATION OF THE PRINCIPLE OF THE PRIN
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Best Local Similarity
Matches 19; Conserv
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Best Local
clone:B1060H01.
Submitted (MAY-
[2]
                                                                                                                                                                                                                                                                 Oryza sativa (Rice), and
Oryza sativa (Japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
B1060H01.30 protein (OSJNBb0021A09.1 protein).
B1060H01.30 OR OSJNBB0021A09.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q90WT9;
Q90WT9;
Q90WT9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
TNF-related apoptosis inducing ligand.
Gallus gallus (Chicken).
Gallus gallus (Chicken).
                                                                                                 Sasaki T., Matsumoto
                                                                                                                        STRAIN=CV. NIPPONBARE;
                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzeae; Oryza. NCBI_TaxID=4530, 39947;
                                                                 "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                        SEQUENCE
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PROSITE; PS50049; TNF_2; 1.
SEQUENCE 287 AA; 32092 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY057941; AAL23702.1; ... InterPro; IPR003436; INE_family. InterPro; IPR00478; INE_family. Pf00229; INE; I...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Bridgham J.T., Johnson A.L.;
"TNF-related apoptosis inducing ligand (TRAIL) expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q90WT9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       771
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                     (MAY-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                   Η.,
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28.8%;
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                                                                                                   Yamamoto K.;
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Pred. No. 29;
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RP SEQUENCE FROM N.A.

RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT TOTYZA SALIVA nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT Clone:OSJNBb0021A09.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP003560; BAB68095.1; -.
DR EMBL; AP003218; BAB89450.1; -.
SQ SEQUENCE 251 AA; 26727 MW; F864DB49AB078164 CRC64;
SQ SEQUENC
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Result
No.
                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein - protein search, using sw model
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
                            Query
                                                                                                                                                                                                                                                                                                                                                                                            112892 seqs, 41476328 residues
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Gapop 10.0 , Gapext 0.5
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373
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 HEAHKTSLSSWKHDQDWANV.....TSAGLTLQDLQLWCNLRIIH 68
                                                                                                                                                                                                                                                                                                                 SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                Length DB
FCG1_MOUSE
TRAP_ECOLI
SLT2_YEAST
                                                                                                                                                          IL1B_TRIVU
YRAN_HAEIN
DISR_AGKRH
                                                                                                                                                                                             TN11_RAT
TN11_MOUSE
PYRF_PICAN
CSD2_DROME
SGAH_ECOLI
                                                                                                                                                                                IPNS_STRCL
Y108_CHLTR
                                                                                                                                            RP1_HUMAN
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                                                                                                                                                                                                                                                                     SUMMARIES
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                                                                                                            014788 h tumor nec Q9ese2 r tumor nec 035335 m tumor nec 035335 m tumor nec Q06375 pichia angu Q9wmt6 drosophila p33304 escherichia p10621 streptomyce 084110 chlamydia t Q9xs77 trichosurus p45300 haemophilus p45300 haemophilus p30403 agkistrodon p25598 saccharomyce p56715 homo sapien p26151 mus musculu p41068 escherichia Q00772 saccharomyce p5528 sulfolobus
                                                                                                                                                                                                                                              Description
                                                                                                     1 mus musculu
8 escherichia
2 saccharomyc
8 sulfolobus
6 hordeum vul
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TNF5_AOTTR
TNF5_CALJA
TNF5_HUMAN
TNF5_MACMU
ATPS_YEAST
NUD1_YEAST
ORC1_KLULA
IPNS_STRJU

P18286

streptomyce

SC65_YARLI IPNS_STRLP ENV_HV1A2 TP11_HUMAN APE2_SULSO
IAAE_HORVU
KALM_HUMAN

SPT6_YEAST

P01086 hordeum vul
P23352 homo sapien
O9ubb9 homo sapien
P2786 oryctolagus
P41922 yarrowia li
P12438 streptomyce
P03378 human immun
P23615 saccharomyc
O9bdm3 aotus trivi

RP RA			RES TN11 ID AC AC DT DT DT DT DT DT OT	
TISSUE-Thy MEDLINE-97. WONG B.R., KALACHÍKOV ChOÍ Y.; "TRANCE ÍS that activ J. Biol. CÚ J. Biol. CÚ J. SEQUENCE EI	Burgess Burlivas Sullivas Sullivas Kaufman Boyle W "Osteop differe Cell 93 [3] SEQUENCI Ikeda T"Detectm Submitte	SEQUENCE F TISSUE-80 MEDLINE-90 Anderson D Tometsko M Galibert I "A homolog and dendri Nature 390 [2] SEQUENCE F TISSUE-Lym	TRISULT 1 TN11_HUMAN TN11_HOMAN T	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
SEQUENCE OF 7 TISSUE=Thymoc MEDLINE=97460 Wong B.R., Rh Kalachikov S. Choi Y.; "TRANCE is a 1 that activate: J. Biol. Chem [5] SEQUENCE FROM TISSUE=Tongue	wan J. van J. va	SEQUENCE FROM N TISSUE-Bone mar MEDLINE-9803297 Anderson D.M., Tometsko M.E., Galibert L.; "A homologue of and dendritic-co Nature 390:175- (2) SEQUENCE FROM N TISSUE-LYMPh noo	_HUMAN TN11_HUMAN O14788; O147 16-OCT-2001 16-OCT-2001 15-JUN-2002 Tumor necros of nuclear finduced cyto differentiat TNFSF11 OR RA HOMO Sapiens ELWARYOta; M Mammalia; Eu NCBL_TaxID-91 [1]	53 55 57 57 57 57 57 57 57 57 57 57 57 57
3-317 ytes; 112; o J., cay, Cay novel s c-J s c-J . 272	Lacey D.L., Timms E. Burgess T., Elliott I Sullivan J., Hawkins Sustantian S., Sarosi I Boyle W.J.; "Osteoprotegerin liga differentiation and cell 93:165-176(1998) [3] SEQUENCE FROM N.A. (J. Ikeda T., Kuroyama H. "Determination of hum Submitted (JUN-2001) [4]	. A round ro	LHUMAN STANE TN11_HUMAN STANE 014788; 014723; Q9P2 16-0CT-2001 (Rel. 4C 15-JUN-2002 (Rel. 4C 15-JUN-2002 (Rel. 41 Tumor necrosis factor of nuclear factor ka induced cytokine) (T differentiation fact TNFSF11 OR RANKL OR HOMO Sapiens (Human) Eukaryota; Metazoa; Mammalia; Eutheria; (1)	14.2 14.2 14.2 14.2 14.2 14.2 14.2
M I	N., Sind in a ctive state of the control of the con	and and skovs skovs E.R. E.R. TNF funct [1997]	ANDARD; 9P2Q3; Q95Q 40, Createe 40, Last s 41, Isast al ctor ligand ctor ligand ctory (ODF DR TRANCE OI nn) 1; Chordata; 1; Primates;	2255 220 334 377 453 475 636 636 764 869 1037
Bar Bar l of ermin 2519	Tan HL Tan HL Colombe Davy E. Shalhoub d is a cyt thvation.' Elivation.' Hirokawa n RANKL is the EMBL	Te Te	Q96Q eate st s st s gand B li B li CE (CD C	4444444444
132; Robinson E., Orlin: tlett F.S. III, Fro the tumor necrosis all kinase in T cell 4(1997).	Dibero A., Elliott G., E., Capparelli C., Senaldi G., Cytokine that regul Dn."; 1: 2 AND 3). wa K.; wa K.; isoforms.";	1). place Discourse Discou	PRT; 317 AA. 17; d) squence update) superfamily member superfamily (TNF- yand) (RANKL) (TNF- yand) (PANKL) (PA	RRPL_SV5 PIS_TEAST GUB_CLOTM PPOB_MEIRU PPAGL_SCHPO PRTG_ERWCH S6A7_HUMAN PAG_BACAN PO21_SCICO BGAL_LACDE YDY2_SCHPO MSH6_YEAST ALIGNMENTS
nkel W.N., Lee S.Y., factor receptor family	<pre>Instan C.R., Scully S., Hsu H., Eli A., Qian YX., Guo J., Delaney J., ates osteoclast tabases.</pre>	Dougall W.C., '., Cosman D., enhance T-cell growth	11 (Receptor activator related activation- and) (OPGL) (Osteoclast ata; Euteleostomi; idae; Homo.	Q88434 simian viru P06197 saccharomyc P29716 clostridium Q92978 meiothermus Q92998 meiothermus P08091 schizosacch Q07162 erwinia chr Q99884 homo sapien P13423 bacillus an Q03279 sciara copr P20043 lactobacill P1013683 schizosacch Q03834 saccharomyc

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by non-profit institute. There are no restrictions modified and this statement is not removed. Usage hy or send an analysis a license agreement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20175237; PubMed=10708588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 formation
                                CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                  CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                              Signal-anchor; Alternative splicing CHAIN 1 317 TUMOR 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                              SMART; SM00207; TNF;
                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00229; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003636; TNF_abc
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
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                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                            PROSITE; PS00251; TNF_1; FALSE_NEG. PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000478;
                                                               VARSPLIC
                                                                                                               CARBOHYD
                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to TNFRSF11A/RANK. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are produced by alternative splicing. TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and secreted (isoform 2). A soluble form of isoform 1 arises by proteolytic processing (By similarity).

ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2/SODF and 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARI
PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
PTM: The soluble form of isoform 1 derives from the mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypercalcemia of malignancy.
SUBUNIT: Homotrimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF019047; AAB86811.1; -..., AF037712; AAC39731.1; -..., AB064269; BAB79694.1; -..., AB061227; BAB71768.1; -..., AB064270; BAB79695.1; -..., AF013171; AAC51762.1; -..., AB037599; BAA90488.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catalyzed by ADAM17
                                                                                                                                                                                                                                                                                                                                                                                                                             602642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB037599; BAA90488.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteolytic processing (By similarity). The cleavage may
                                                                                                                                                                                                                                                                                                                                                                                                                                           HGNC:11926; TNFSF11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biophys. Res. Commun. 269:532-536(2000)
                                                                                                                                                                                                                                                                                             Differentiation; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                 140
                                                                                                 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1D0G
                                                                                                                                                                                                                                                                                                                                                              TNF_abc; 1.
                                                                    140
171
198
47
73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         license agreement (See http://www.isb-sib.ch/announce,
                                     35478 MW;
                                                                                                                                                                                                                                                                                                                                                                                              TNF_family.
   47.78;
                                                                CLEAVAGE (BY SIMILARITY).

"-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

MISSING (IN ISOFORM 3).

MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                MEMBER 11, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11, SOLUBLE FORM (BY SIMILARITY).
      Score 178;
                                                    A -> G
                                                                                                                                                                                 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                 CYTOPLASMIC
                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                       766176446348097F CRC64;
                                                        (IN REF.
                                                                                                                                                                                                    (POTENTIAL)
      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from the membrane
      Length 317;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last sequence update)
16-JUN-2002 (Rel. 41, Last sequence update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning, sequence and functional characterization of the rat homologue of receptor activator of NF-kB ligand.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20540945; PubMed=11092398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Odgren P.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Fischer 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 266-318 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the TNFSF11 (TRANCE, RANKL, ODF, OP
Int. J. Dev. Biol. 45:853-859(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marks S.C. Jr.;
"Evidence that the rat osteopetrotic mutation toothless (tl) is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11804028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zheng M.H.;
                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                              InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
                                                                                        HSSP;
                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                   entities
                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                    between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to TNFRSF11A/RANK. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rissue specificity: Highly expressed in thymus and bone rissue specificity: Highly expressed in thymus and bone by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypercalcemia of malignancy.
SUBUNIT: Homotrimer (By similarity)
                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration entry is copyright. It is produced through a collaboration to the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics.
                                                                                        P50591;
                                                                                                                                           AF187319;
                                                                                                                   AF425669;
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                                                                                                                                                                                                                             requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                    AAG17031.1; -.
                                                                                                                   AAL23963.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    II membrane protein and secreted (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPGL) gene.";
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Pfam; PF00229;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00251; TNF_1; FALSE_NEG PROSITE; PS50049; TNF_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
11-JUN-2002 (Rel. 40, Last sequence update)
11-JUN-2002 (Rel. 40, Last annotation update)
11-JUN-2002 (Rel. 40, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TN11_MOUSE STANDARD; PRT; 31
035235; 035306; Q9R1Y0; Q9JJK8; Q9JJK9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence upd.
15-JUN-2002 (Rel. 41, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gnal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 SHKVSLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPADYLQL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THESE 11 OR RANKL OR TRANCE OR OPGL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97460112; PubMed-9312132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AHKTSLSSWKHDQDWANVSNMTESNGKLRVK--GIVYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                           Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Thymic lymphoma;
MEDLINE-98032977; PubMed-9367155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1)
Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
                                                                                                    TISSUE=Bone marrow;
MEDLINE=98227661; PubMed=9568710;
                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                     Nature 390:175-179(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD002012; TNF_abc; 1.
                                                                                                                                                                                                                                                                                                  homologue of the TNF receptor and its ligand enhance T-cell growth
                                                                                                                                                                                                                                                                            dendritic-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pifferentiation; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318
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140
199
264
317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272:25190-25194(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.9%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                           function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4B87A4D706AD098F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M., Murakami A., Tsuda E., Mochizuki S. I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E., Mochizuki S. I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E., Mochizuki S. I., Higashio K., Udagawa N., Takahashi N., Suda T., "Osteoclast differentiation factor is a ligand for "Osteocratat differentiation factor is a ligand for costeoprotegerin/osteoclastogenesis-inhibitory factor and is identical to TRANCE/RANKL.";

proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differentiation and activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Bone marrow stroma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell 93:165-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ueda M., Higashio K.; "Cloning and characterization of the gene encoding mouse osteoclast differentiation factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99214075; PubMed=10196481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 230:121-127(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ikeda T., Kasai M., Utsuyama M., Hirokawa K.; "Determination of three isoforms of the receptor activator of nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H., Schloendorff J., Tempst P., Choi Y., Blobel C.P., Erdjument Bromage H., Evidence for a role of a tumor necrosis factor alpha "Evidence for a role of a tumor necrosis factor alpha (TNF-alpha)-converting enzyme-like protease in shedding of TRANCE, a TNF family member involved in osteoclastogenesis and dendritic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endocrinology 142:1419-1426(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor-kappaB ligand and their differential expression in bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         survival.
                                                                                                                                                                                                                                                                                                         J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.; recrystal structure of the TRANCE/RANKL cytokine reveals determinants of receptor-ligand specificity."; of receptor-ligand specificity."; J. Clin. Invest. 108:971-979(2001).
                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316
PubMed=11733492;
                                                                                                                                                                                                                                                                                                                                                         Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.; "Crystal structure of the extracellular domain of mouse RANK ligand at
-i- SUBCELLULAR LOCATION: Type II membrane protein and secreted
(1soform 1 and 2); Cytoplasmic (1soform 3); are
(1soforms 1 and 2); alsoforms; 1 (shown here), 2 and 3; are
-i- ALTERNARIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; are
-i- produced by alternative splicing.
-i- produced by alternative splicing.
-i- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THEMUS AND LYMPH NODES BUT
-i- NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN THE
BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 274:13613-13618(1999).
                                                                                                                                                                                                                                                                                                                           -A resolution.";
Biol Chem. 277:6631-6636(2002).
                                                                                                                                                                                                                                                             JIOI. Chem. 277:6631-6636(2002).

FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to FUNCTION: Cytokine that binds to TNFRSF11A/RANK. Osteoclast differentiation and activation factor. TNFRSF11A/RANK. Osteoclast differentiation and incomments the ability of immovement recommendator of interactions augments the ability of immovement recommendator of interactions.
                                                                                                                                                                            proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral
                                                                                                                                                               hypercalcemia of malignancy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
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RESULT 4
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                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE: PS00251; TNF_1; FALSE_NEG.
PROSITE: PS00251; TNF_2; 1.
Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
Signal-anchor; 3D-structure; Alternative splicing; Transmembrane;
CHAIN 1 316
MEMBER 11, MEMBRANE FORM,
MEMBER 11, MEMBRANE FORM,
CHAIN CIDERFAMILY
                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00229; TNF; 1.
SMART; SM00207; TNF; 1
                                                            3 AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PTM: N-91ycosylated.
-!- PTM: The soluble form of isoform 1 derives from the membrane form by proteolytic processing. The cleavage may be catalyzed by proteolytic processing. The cleavage may be catalyzed by ADAMI. A further shorter soluble form was observed.
-!- DISEASE: DEFICIENCY IN TWESF11 RESULTS IN FAILURE TO FORM LOBULO-OF NEWBORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPETROSIS, WITH PROFOUND GROWTH RETARDATION AT SEVERAL STEERS ON THE LIMBS, SKULL, AND VERTEBERAE AND HAVE MARKED CHONDRODYSELASTA, WITH THE LIMBS, SKULL, AND VERTEBERAE AND HAVE MARKED CHONDRODYSELASTA, HYPERTROPHIC CHONDROCYTES.
-!- STMILABITY. REFUNDES TO THE THMOR NEFFORTS FAMTIVE INCREASE IN
                                                                                                                                                                           oca1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content in in oway modified and this first are the content in the same time of the content in the content i
                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:1100089; Tnfsf11.
rPro; IPR003636; TNF_abc.
rPro; IPR000478; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1JTZ; 12-SEP-U1.
1IQA; 13-MAR-02.
                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRABECULAR BONE AND LUNG.
                                                                                                                                                                                                                                   316 AA;
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNF; 1.
                                                                                                                                                          46.18;
56.78;
                                                                                                                                                                                                                              34944 MW;
                                                                                                                                       6,
                                                                                                                                     Score 172; Db 1,
No. 4.4e-14;
                                                                                                                                                                                                                                        G -> D (IN REF. 2).
MISSING (IN REF. 5)
                                                                                                                                                                                                                                                                                   SSEEMGSGPGVPHEGPLHPAPSAPAPAPAPPPA -> TP (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11, SOLUBLE FORM.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                        08DF63A2BE00967A CRC64;
                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                       LINKED
                                                                                                                                                                                                                                                                                                              O (GLCNAC. .) (POTENTIAL).
(IN ISOFORM 3).
                                                                                                                                                          DB 1; Length 316;
                                                                                                                           18;
                                                                                                                 Indels
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CSD2
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ID PYRE_PJ
AC Q06375;
DT Q1-JUN-
Q1 15-JUN-
DT 15-JUN-
DT 15-JUN-
DT 15-JUN-
DT 01-JUN-
DT 15-JUN-
DT 01-JUN-
DT 15-JUN-
DE SYNTHAS
GN URA3;
GN MEDLINI
RI Hansen,
RI Hansen,
RI Hansen,
RI Hansen,
GC -1- PAJ
GC -1- PAJ
GC -1- PAJ
GC -1- PAJ
GC This SY
GC Detweer
GC This SY
GC GOT SEN
GC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                          MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.. Amanatides P.G., Scherer S.E., Li
                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
Probable cytochrome P450 28d2 (EC 1.14. --) (CYPXXVIIID2).
CYP28D2 OR CG5081.
Drosophila melanogaster (Fruit fly).
Drosophila Mctannogaster (Fruit fly).
                                                                                                                STRAIN=Berkeley
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9VMT6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSD2_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S31323; S31323.
HSSP; P03962; 1DQW.
InterPro; IPR001754; OMPdecase.
Pfam; PF00215; OMPdecase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrimidine biosynthesis; Lyase; Decarboxylase.
ACT_SITE 92 92 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00156; OMPDECASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 DRKFADIGNTV----KLQYKĞGIYRTSKWADITNAHGVTGAĞI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 DQDWANVSNMTFSNGKLRVKGIYYRN---ADICSRHRVTSAGL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Merckelbach A., Goedecke S., Janowicz Z.A., Hollenberg C.P., "Cloning and sequencing of the ura3 locus of the methylotrophic yeast Hansenula polymorpha and its use for the generation of a deletion by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94128354; PubMed=7764392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-UN-1994 (Rel. 29, Created)
01-UN-1994 (Rel. 29, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Orotidine 5'.phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)
(OMPDCase) (OMPdecase) (Uridine 5'.monophosphate synthase) (UMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRF_PICAN
Q06375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                  Celniker S.E., Holt R.A., Ev
P.G., Scherer S.E., Li P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 AA; 29275 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               les; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 63.5; DB 1; ]
Pred. No. 1.2;
7; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0934EF673B03A820 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
Evans C.A., Gocayne J.D.,
'., Hoskins R.A., Galle R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             501 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetes;
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Query Match
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            George R.A.,
Sutton G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished observations (SEP-2000).

-i- FUNCTION: MAY BE INVOLVED IN THE METABOLISM OF INSECT HORMONES AND IN THE BREAKDOWN OF SYNTHETIC INSECTICIDES (BY SIMILARITY).

-i- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                            FlyBase; FBgn0031688; Cyp28d2
                                                                                                                                                                                                                                                                                                        EMBL; AE003609; AAF52225.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ONCEPTUAL TRANSLATION.
                                                                                                                 Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome; Endoplasmic reticulum; Hypothetical protein.
BINDING 446 446 HEME (BY SIMILARITY).
                                                                                                                                                                                          PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                    Pfam; PF00067; P450; 1.
                                                                                                                                                                                                                                                           InterPro;
                                                                                             SEQUENCE
                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Potential).
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oxidized flavoprotein + H(2)0.
SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAUTION: Ref.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ., Wortman J.R.,
                                                                                                                                                                                                                                                           IPR001128; Cytochrome_P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lewis S.E., Richards S., Ashburner M., Henderson S.N., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Rogers Y.-H.C., Blazej R.G., Champe B. Willow T. G.
                                                                                               501 AA;
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence differs from that shown due to erroneous
                                                                                                    58222 MW;
                                20.8%;
                                                    16.5%;
          11;
                           Score 61.5;
Pred. No. 4
          Mismatches
                                                                                                    9AD85F249390A655 CRC64;
                                                         DB 1;
            34; Indels 35;
                                                         Length 501;
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SGAH_ECOLI
ID SGAH_I
AC P3930
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                            Query Match
 Best Local
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P39304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
probable hexulose-6-phosphate synthase (EC 4.1.2.-) (HUMPS) (D-arabino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-hexulose 6-phosphate formaldehyde lyase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reizer J., Charbit A., Reizer A., Saier M.H. Jr.;
"Novel phosphotransferases system genes revealed by bacterial genome analysis: operons encoding homologues of sugar-specific permease domains of the phosphotransferase system and pentose catabolic enzymes.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGAH OR B4196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95334362; PubMed=7610040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 YPVSQSVCKKFVEYIRRQQQMATSEGLDAMDLSLCYTTEVV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region from 92.8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Analysis of the Escherichia coli genome VI: DNA sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 YYRNADICSR-----HRVTSAGLTLQDLQLWCNLRII 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 HKTYATDFRSF-HNNEWRNFVNKKTDMILGNNPFVLTGDEWKERRSEIMPALSPNRVKAV 151
                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: PROBABLY PART OF A SUGAR METABOLIC PATHWAY ALONG WITH
                                                                                                                                                                                                                                                                                                                                                                            -1- FUNCTION: CONDENSATION OF D-RIBULOSE 5-PHOSPHATE WITH FORMALDEHYDE TO FORM D-ARABINO-6-HEXULOSE 3-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                              Microbiology 143:2519-2520(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Is the ribulose monophosphate pathway widely distributed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reizer J., Reizer A., Saier M.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97419490; PubMed=9274005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISCUSSION OF SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enome sci. Technol. 1:53-75(1996).
                                                                                                      SWISS-2DPAGE; P39304; COLI.
EcoGene; EG12496; sgaH.
InterPro; IPR001754; OMPdecs
                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE HUMPS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HEAHKTSLSSWKHDQDWANVSN----MTFSNGKL-----
                                                                                                                                                                        EMBL; U14003; AAA97092.1; -.
                                                            SEQUENCE
                                                                                            Pfam; PF00215; OMPdecase; 1.
                                                                                                                                                                                                                                                                                                                                                    SGAU AND SGAE
                                                                                                                                                            AE000491;
l Similarity
17; Conserv
                                                                             Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / MG1655;
                                                                 216 AA;
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                           AAC77153.1; -
                                                                 23578 MW;
                  16.0%;
                                                                                                                 OMPdecase.
     16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                    Score 59.5; Di
Pred. No. 3.1;
                                                                   EC8490DA1D02D824 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 AA
                                      DB 1; Length 216;
                                                                                                                                                                                                                                                             as its content
                                                                                                                                                                                                                                             Usage
          Indels 11;
                                                                                                                                                                                                                                               ру
                                                                                                                                                                                                                                                  and
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A TO THE TERM OF T
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Дb
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                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                         METAL
                                                                                                                                                                                                                                                                                              Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin METAL 212 212 IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00185; IPNS_1; 1. PROSITE; PS00186; IPNS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR005123; 20G-FeII_Oxy.
InterPro; IPR002283; IPN_synth.
InterPro; IPR002057; Isopen_N_synth.
Pfam; PF03171; 20G-FeII_Oxy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way the state of the sta
                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00682; IPNSYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M19421; AAA26770.1; -. EMBL; A01132; CAA00131.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and nucleotide sequence determination of the isopenicillin N synthetase gene from Streptomyces clavuligerus.";

Gene 62:187-196(1988).

-I FUNCTION: REMOVES, IN THE PRESENCE OF OXYGEN, 4 HYDROGEN ATOMS FORM THE AZETIDINONE AND THIAZOLIDINE RINGS OF ISOPENICILLIN.

COPACTOR: IRON AND ASCORBATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A29894; A29894.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: CENTRAL ROLE IN THE BIOSYNTHESIS OF PENICILLIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 27064 / DSM 738 / NRRL 3585;
MEDLINE-88212175; PubMed-3130293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leskiw B.K., Aharonowitz Y., Mevarech M., Wolfe S., Vining L.C., Westlake D.W.S., Jensen S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobactéria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces,
                              1 HEAHKTSLSSWKHD------QDWANVSNMTFS--NGKLRVKGIYYRNADICSRHRVTSA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces clavuligerus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P10621;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isopenicillin N synthetase (EC 1.-.-) (IPNS) (Isopenicillin N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 LEDLPLFKGIPI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 TGYWTWEQAQQWRDAGIGQVVYHRSRDAQAAGVAWGEADITAIKRLSDMGFKVTVTGGLA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEPHALOSPORIN.
SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P05326; 1BLZ
                                                                                                                        18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSLSSWKHDQDW--ANVSNMTFSNGK-LRVKGIYYRNADICSRHRVT-----SAGLT 54
                                                                                                                                             Similarity
                                                                                                                                                                                                                                 329 AA;
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                        268
36958 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomycineae; Streptomycetaceae;
                                                                                                                                          16.0%;
25.7%;
                                                                                                10; Mismatches
                                                                                                                                    Score 59.5;
                                                                                                                                                                                                                                           IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
                                                                                                                                                                                                            71AA1CCE9514761C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 AA
                                                                                                                                                         DB 1;
                                                                                                   33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
                                                                                                                                                         Length 329;
                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and for
                                                                                                9
                                                                                          Gaps
                                                                                          2
S C C C S D D D D
                                                                                                                                                                                                                                                                                                                                              RESULT 9
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Y108_CHLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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Query Match
                                             Trichosurus vulpecula (Brush-tailed possum)
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Metatheria; Diprotodontia; Phalangeridae;
                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Interleukin-1 beta precursor (IL-1 beta).
NCBI_TaxID=9337;
                                                                                                                                                                                     IL1B_TRIVU Q9XS77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
SEQUENCE 251 AA; 27474 MW; A4C2F6BE7517298E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002678; DUF34. Pfam; PF01784; DUF34; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                     162 ALGGKKRVSSAAL 174
                                                                                                                                                                                                                                                                                                                                                                    102 DAHTTIGNNWKVARDLGWEQLESFGSSQPSLGVKGVFPEMEVHDFISQLSAYYQTPVLAK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGRO0486; DUF34; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHCI-2DPAGE; 084110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001284; AAC67699.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y108_CHLTR
084110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 282:754-759(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., An Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                              44 ---SRHRVTSAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99000809; PubMed=9784136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=D/UW-3/Cx;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein CT108.
                                                                                                                                                                                                                                                                                                                                                                                                           2 EAHKTSLSSWK--HDQDWANVSNMTFSNGKLRVKGI------YZRNADIC- 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 GTPMHEVNLW 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 GLTLQDLQLW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 NEFHGAMTDQEKHDLAIHAYNPDNPHVRNGYYKAVPGRKAVESFCYLNPDFGEDHPMIAA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 40, Last sequence update)
                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.7%;
26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 58.5; DB
                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                              269 AA
                                                                                                              update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
  Trichosurus.
                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS

C. OR IS SEQUENCE SUGGESTS THAT IL-1 IS SEGMENT IN THE SELLARDIN AMONGED BY A MECHANICA METERATION AND ARE REPORTED TO STIMULATE OF MATURATION AS ENDOGENOUS PROCESS, AND ARE REPORTED TO STIMULATE OF THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.

C. ISUBUNIT: MONOMER.

C. AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

C. AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

C. AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

C. AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

C. OR TS SERVERSON SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS.

C. OR TS SERVERSON AMECHANICA ETERPTON TO OTHER PROCESSION OF THE MECHANICA METERPETING FOR METERSON METERSON METERPETING FORM METERSON 
                                                                                                                                                                                                                                                                                                               RESULT 10
YRAN_HAEIN
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  ROCCOS GE DIT DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002348; IL1_HBGF.
InterPro; IPR003502; IL1_propep.
InterPro; IPR000975; Interleukin_1.
pfam; pf00340; IL1; 1.
pfam; pf002394; IL1_propep; 1.
prinys; pr00256; IL1HBGF.
prinys; pr00256; IL1HBGF.
proDom; pp002556; Interleukin_1; 1.
smarT; sm00125; IL1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modifies requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF071539; AAD21871.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01584; 1HIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine; Macrophage; Mitogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                    P45300;
                                                                            Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                     Haemophilus influenzae
                                                                                                                                                        Hypothetical protein HI1656.
                                                                                                                                                                                                                                                                                           YRAN_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                       117 DSSFRLVSSQDCTIQDINQKCLALSKASELRALH 150
NCBI_TaxID=727;
                                                Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 HQFHQTVMVIVAIEKMKHLNGLSSQFFQDNDLMNIFTNIFQE----EPITEKNCDIYES 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 -CSRHRVTSAGLTLQDLQLWC-----NLRIIH 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HEAHKT-----SLSSWKH------DQDWANVSNWTFSNGKLRVKGIYYRNADI--- 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECRETORY PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31141 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.7%;
24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n; Inflammatory response; Pyrogen
By SIMILARITY.
INTERLEUKIN-1 BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58.5;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307A1FE3B627D6E7 CRC64;
                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                               119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31;
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RESULT 11
DISR_AGKRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95350630; PubMed=7542800;
Rleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Weidman J.F., Phillips C.A., Spriggs T., Beoghagen N.S.M., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Fine L.D., Fritchman J.L., Small K.V., Fraser C.M., Smith H.O., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-Rd / KW20 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long using the sum of the statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE UPF0102 FAMILY. STRONG, TO E.COLI YRAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U32838; AAC23300.1; -. TIGR; HI1656; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGRO0252; TIGRO0252; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Complete proteome.
SEQUENCE 119 AA; 13812 MW; B7359D8181F31AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02021; UPF0102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
Hemorrhagic protein-rhodostomin precursor (EC 3.4.24.-) (RHO)
                                                                                                                                                                                                                                                                                                                                                                                                                 Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
Eukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P30403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISR_AGKRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 Q-W 113
                                                                                                                                                                                                                            TISSUE=Venom gland;
MEDLINE=93277962; PubMed=7916635;
                                                                                                                                                                                                                                                                                                                                      Viperidae; Crotalinae; Calloselasma.
NCBI_TaxID-8717;
                                                                                                         precursor of platelet aggregation inhibitor and hemorrhagic protein from Calloselasma rhodostoma venom.";
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contains: Disintegrin rhodostomin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 HSAYGSAIESVDWRKOOKWLDAANLWLAKONMSLE-----DANCREDLIAFGKTPODI 111
      TISSUE=Venom gland
                           SEQUENCE OF 77-478 FROM N.A.
                                                                                       Biochim.
                                                                                                                                                                "Nucleotide sequence of a full-length cDNA encoding a common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 QLW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KW20 / ATCC 51907
                                                                                    Biophys. Acta 1173:243-245(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.5%;
23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UPF0102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 58; DB 1; Length 119; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 AA
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Pfam; PF00200; disintegrin; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
PRINTS; PR00289; DISINTEGRIN.
PRODOM; PD000664; Disintegrin; 1.
SMART; SM00050; DISIN; 1.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50214; DISINTEGRIN_2; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                  DISULFID
                                 METAL
                                                                             METAL
                                                  METAL
                                                                                                                            PROPEP
                                                                                                                                                            PROPEP
                                                                                                                                                                         SIGNA
                                                                                                                                                                                  Hydrolase; Metalloprotease; Zinc; Blood coagulation; Platelet;
                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000133; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L08780; AAA49196.1; -.
PIR; JQ1301; JQ1301
PIR; S33792; S33792.
HSSP; P17494; 1KST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; M12.161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTS IN HEMORRHAGE.

-I- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACT BY BINDING TO THE GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91046142; PubMed=2236100;
Gould R.J., Polokoff M.A., Friedman P.A., Huang T.-F., Holt J.C.,
Cook J.J., Niecviarowski S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Disintegrins: a family of integrin inhibitory proteins from viper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 408-475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Au L.-C., Huang Y.-B., Huang T.-F., Teh G.-W., Lin H.-H., Choo K.-B., Acommon precursor for a putative hemorrhagic protein and rhodostomin, a platelet aggregation inhibitor of the venom of calloselasma rhodostoma: molecular cloning and sequence analysis."; Biochem. Biophys. Res. Commun. 181:585-593(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thang H.H., Hu S.T., Huang T.-F., Chen S.H., Lee Y.H., Lo S.J., "Rhodostomin, an RGD-containing peptide expressed from a synthetic gene in Escherichia coli, facilitates the attachment of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93135775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92095959; PubMed=1755841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 408-475 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: BINDS ONE ZINC ION.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
SIMILARITY: CONTAINS 1 DISINTEGRIN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biophys. Res. Commun. 190:242-249(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXP. Biol. Med. 195:168-171(1990).
ON: THIS PROTEIN IS A ZINC PROTEASE FROM SNAKE VENOM THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=7916592;
                                                                                                                                                                              Zymogen;
ZINC (CATALYTIC) (PROBABLE).
BY SIMILARITY.
ZINC (CATALYTIC) (PROBABLE).
ZINC (CATALYTIC) (PROBABLE).
BY SIMILARITY.
                                                                                                 RHODOSTOMIN
                                                                                                                            HEMORRHAGIC PROTEIN
                                                                                                                                                  POTENTIAL
                                                                                                                                                               POTENTIAL.
                                                                                                                                                                   Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Choo K.-B.;
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                                                                                            "RNA14 and RNA15 proteins as components of a yeast pre-mRNA 3'-end processing factor."; Science 266:1702-1705(1994).
-!- FUNCTION: COMPONENT OF THE CLEAVAGE FACTOR I (CF I) INVOLVED IN PRE-MRNA 3'-END PROCESSING. INTERACTS WITH FIP1 AND PROBABLY AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
Devlin K., Churcher C.M.,
                                                                                                                                                                         Minvielle-Sebastia L., Preker P.J., Keller
                                                                                                                                                                                    MEDLINE=95084159; PubMed=7992054;
                                                                                                                                                                                                              FUNCTION.
                                                                                                                                                                                                                       Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                          Minvielle-Sebastia L., Winsor B., Bonneaud N., Lacroute F., Mutations in the yeast RNA14 and RNA15 genes result in an abnorm mRNA decay rate, sequence analysis reveals an RNA-binding domain the RNA15 protein.",
                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 28583 / FL100;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 28583 / EL100;
MEDLINE-91246175; PubMed-1674817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RN14_YEAST
P25298;
                                                                                                                                                                                                                                                                                                                                               REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyceta.

NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1992 (Rel. 22, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
mRNA 3'-end processing protein RNA14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA14 OR YMR061W OR YM9796.14.
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                                                           SUBCELLULAR LOCATION: NUCLEAR AND/OR CYTOPLASMIC SIMILARITY: CONTAINS 6 HAT REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 YKYMHFGISLVNLETWCNGDLIN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 TNWESDEPIKKYSQLNLNHEIKRHYDIYYYVDSRFCTKHSNDLEVIRKFYHEVVNAIIES 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 -----GLTLQDLQLWCNLRIIH 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                               Cell. Biol. 11:3075-3087(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 SSWKHDQDWANVSNWTFSNG-KLRVKGIYYRNADICSR-----HRVTSA----
                                                                                                                                                                                                                                                                                        (JUL-1994) to the EMBL/GenBank/DDBJ databases
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478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.4%;
20.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54006 MW;
                                                                                                                                                                                                                                 Barrell B.G., Rajandream M.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   677 AA.
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                                                                                             PROBABLY ALSO
                                                                                                             INVOLVED IN
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Matches
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P56715;
                                                                                   "A nonsense mutation in a novel gene is associated with pigmentosa in a family linked to the RPI locus."; Hum. Mol. Genet. 8:1541-1546(199).

-i- FUNCTION: COULD HAVE A ROLE IN THE DIFFERENTIATION
                                                                                                                                                                                                                                                                                                       Pierce E.A., Quinn T., Meehan T., McGee T.L., Berson "Mutations in a gene encoding a new oxygen-regulated protein cause dominant retinitis pigmentosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sullivan L.S., Heckenlively J.R., Bowne S.J., Zuo J., Hide W.A., Gal A., Denton M., Inglehearn C.F., Blanton S.H., Daiger S.P., "Mutations in a novel retina-specific gene cause autosomal dominant retinitis pigmentosa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Oxygen-regulated protein 1 (Retinitis pigmentosa
(Retinitis pigmentosa 1 protein).
                                                                                                                                                                      Guillonneau X., Piriev N.I., Danciger M., Kozak C.A., Cideciyan A.V., Jacobson S.G., Farber D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                      MEDLINE=99330563; PubMed=10401003;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99318095; PubMed=10391211;
                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99318096; PubMed-10391212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                              PHOTORECEPTOR CELLS.
TISSUE SPECIFICITY:
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AT 56 88 HAT 2
AT 90 124 HAT 2
AT 138 170 HAT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z49703; CAA89771.1;
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15; Conserv
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138
181
257
298
677 AA;
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124 H
170 H
214 H
289 H
330 H
79960 MW;
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Pred. No. 21;
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HAT
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N RETINA. NO.
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                                           NOT EXPRESSED
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                                                                                                                                                                                                                                                                                                                              E.L., Dryja T
photoreceptor
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                                                                                                                                                        retinitis
                  SPLEEN AND
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PLACENTA,

LUNG,

LIVER,

SKELETAL

KIDNEY,

DI DI DE

1_MOUSE FCG1_MOUSE P26151; 01-MAY-1992 01-MAY-1992 15-JUN-2002

STANDARD;

PRT;

404

A

High affinity immunoglobulin gamma

(Rel. 22, Created)
(Rel. 22, Last sequence update)
(Rel. 41, Last annotation update)
(Rel. 41, Last annotation update)

RESULT

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                                                                                                                                  Matches
                                                              Query Match
Best Local
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EMBL; AF143225; AAD44197.1; J
EMBL; AF143225; AAD44198.1; -
EMBL; AF143222; AAD44198.1; -
EMBL; AF141021; AAD42072.1; -
EMBL; AF152242; AAD46774.1; -
EMBL; AF152240; AAD46774.1; J
EMBL; AF152241; AAD46774.1; J
EMBL; AF146592; AAD46769.1; -
                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                            InterPro; IPR003533; DC Pfam; PF03607; DCX; 2. SMART; SM00537; DCX; 2.
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                      6 TSLSSWKHDQDWANVSNMTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQD
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DISEASE: DEFECTS IN RP1 CAUSE RETINITIS PIGMENTOSA FORM 1 (RP1); IDISEASE CHARACTERIZED BY CONSTRICTION OF THE VISUAL FIELDS, NIGHT BLINDNESS, AND FUNDUS CHANGES. THE DISEASE SEEMS TO BE ASSOCIATED WITH TRUNCATED (STOP OR FRAMESHIFT MUTATIONS) FORMS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WWW="http://www.sph.uth.tmc.edu/retnet/".
DATABASE: NAME=Mutations of the RP1 gene;
NOTE-Retina International's Scientific Newsletter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WWW="http://www.retina-international.com/sci-news/rp1mut.htm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DATABASE: NAME-RetNet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 2 DOUBLECORTIN DOMAINS
SSVASKKKKKSRQQAINSRYQDGQLATKGILNKNERINTKGRITKE-MIVQD
                                                                                                                                                                                                                                                                                                                                                             603937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE=Retinal information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF143226; AAD44197.1;
                                                 l Similarity
15; Conser
                                                                                                                                                                                                                                                                                                                                                                       HGNC:10263; RP1.
                                                                                                                                                                                                                                                                                        Retinitis
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154
268
671
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872
                                                Conservative
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                                                          15.4%;
                                                                                              240659 MW;
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                                                         Score 57.5;
Pred. No. 81;
                                                                                                                    /FTId=VAR_007813
C -> Y
                                                                                                                                                                                          /FTId=VAR_007810
N -> Y
                                                                                                                                            Ś
                                                                                             /FTId=VAR_007814.
W; 55AEDBEC43D6A507 CRC64;
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                                                                                                                                                                                                                                                                                     Polymorphism; Repeat.
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                                               Mismatches
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716
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                                       Query Match
Best Local
                             Matches
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Osman N., Kozak C.A., McKenzie I.F., Hogarth P.M.;
"Structure and mapping of the gene encoding mouse high affinity
gamma RI and chromosomal location of the human Fc gamma RI gene.
J. Immunol. 148:1570-1575(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                DISULFID DISULFID
                                                                                                                                                                                                                           TRANSMEM
DOMAIN
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PIR; A46480; A46480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- TISSUE SPECIFICITY: MACROPHAGE-SPECICIC.
-i- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-i- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor
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SMART; SM00408; IGC2; 1.
IgG-binding_protein; Receptor;
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M31314; AAA40056.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sears D.W., Osman N., Tate B., McKenzie I.F.C., Hogarth P.M.; "Molecular cloning and expression of the mouse high affinity Fc receptor for IqG.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90111035;
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P41068;
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                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Shimizu H., Saitoh Y.,
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m SWISS\text{-}PROT} entry is copyright. It is produced through a collaboration een the {
m Swiss} Institute of Bioinformatics and the EMBL outstation -
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ALIGNMENTS	A46480 C96831 T34395 S73098 S43737 S73098 AF0122 B90674 E85524 T1BH 148471 148471 T09366 A40351 A40351 S17982 T06291
ENTS	Fc gamma (IgG) rec hypothetical prote hypothetical prote hypothetical prote protein kinase SLT aminopeptidase (EC probable membrane Aida-I adhesin-lik probable beta-barr trypsin inhibitor Fc gamma (IgG) rec cytochrome P450 ho adhesion-type prot Kallmann syndrome extensin homolog T hypothetical prote

conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Acces: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: E72203
C;Accession: E72203
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi. R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.S.; Phillips, C.A.; Richardson, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,

Hic

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316; PMID:10360571

Nature 399, 323-329, 1999

A; Accession: E72203

A; Status: preliminary

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A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TML852
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-296 <ARN>
A;Cross-references: GB:AE001822; GB:AE000512; NID:g4982429; PIDN:AAD36914.1; PID:g498
                                                                                                                                                                                                                                           R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; submitted to the Protein Sequence Database, January 2000 A;Reference number: Z23021 A;Accession: T46103
                                                                                                                                                                                                                                                                                                                                   hypothetical protein T25B15.100 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T46103
                                          A; Map position: 3
A; Introns: 63/3; 7
A; Note: T25B15.10
                                                                                                                                A; Experimental source: cultivar Columbia; BAC clone T25B15
                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-307 <ALC>
A;Cross-references: EMBL:AL132972
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C; Superfamily: or C; Keywords: carbo F; 3-263/Domain: o
probable siderophore receptor PA1365 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
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A;Description: Cloning and sequencing of the URA3 locus of the methylotrophic yeast Hans A;Reference number: S31323
A;Accession: S31323
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-263 <M
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C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000 C:Accession: S31323
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J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable glucanotransferase (endo alpha-1,4 polygalactosaminidase related protein) [impd C:Species: Clostridium acetobutylicum C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C:Accession: E96990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CAC0736
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A:Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-276 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 NWK-DESWIDVSNIKWDNYVVNTIGKNIKNKGVDGFFIDNIDVYSKYKKDSMFIGIINI 162
                                                                                                                                                       90 DRKFADIGNTV----KLOYKGGIYRTSKWADITNAHGVTGAGI 128
                                                                                                                                                                                                 14 DQDWANVSNMTFSNGKLRVKGIYYRN---ADICSRHRVTSAGL 53
                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 SWKHDQDWANVSNMTFSN-----GK-LRVKGI---YYRNADICSRHRVTSAGLTLQDL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 ADICSRHRVTSAGLTLQDLQLW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HEAHKTSLSSWKHDQDW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HDEYKVLSFIWRHNKEWKVRSEHHVLVLGARTSWKKTQCHIHHLPYSQG-ITINGVLYYG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AWTDDKCVLMSFDLTSEDVGVW 229
                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                   1-263 <MER>
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                  17.0%;
39.5%;
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30.5%;
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                                                                                                                                                                                                                                                                     Score 63.5;
Pred. No. 5.
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Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 2.3;
9; Mismatches
                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                          DB 1; Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 276;
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                A; Experimental source: clone Y70C5D C; Genetics:
                                                                                                                                              A;Reference number: Z20352
A;Accession: T27354
                                                                                                                                                                                                                    R;Steward,
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: clone T25E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: Z20009
A; Accession: T25282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Matthews,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: clone F14D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: Z19339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-813 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: strain PAO1
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A;Molecule type: DNA
A;Residues: 1-1101 <WI4>
A;Cross-references: EMBL:AL021507; PIDN:CAA16430.1; GSPDB:GN00023; CESP:T25E12.4a
                                                                                                                                                                                                                                                                                                                                                                                                    R; Barlow, K. submitted to the EMBL Data Library, January 1998 A; Reference number: Z20182 A; Accession: T26254 A; Accession: T26254
                                                                                                                                                                                                     submitted to the EMBL Data Library, January 1998
                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-1101 <WI3>
A;Cross-references: EMBL:AL021572; PIDN:CAA16519.1; GSPDB:GN00023; CESP:T25E12.4a
                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-1101 <WIZ>
A; Cross-references: EMBL: Z82052; PIDN: CAB04830.1; GSPDB: GN00023; CESP: T25E12.4a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, November 1996
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A;Residues: 1-1101 <WTL>
A;Cross-references: EMBL:Z92967; PIDN:CAB07478.1; GSPDB:GN00023; CESP:T25E12.4a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  711 TAYLQYKPDADWNNRLQATFFDSKDYRLDGVESFGRRQVSTYTTVDLVSQYRITPDDQLS 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSLSSWKHDQDWANVSNMTFSNGK-LRVKGI-----YYRNADICSRHRVT---SAG 52
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28.8%; Pred. No. 19;
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A;Introns: 13/3; 77/1; 98/2; 201/1; 263/3; 310/1; 398/3; 440/3; 469/3; 506/1; 541/1; 571 C;Superfamily: protein kinase C zinc-binding repeat homology <KZN1>F;322-371/Domain: protein kinase C zinc-binding repeat homology <KZN2>F;474-523/Domain: protein kinase C zinc-binding repeat homology <KZN2>
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC1866...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
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A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: a110476
C;Superfamily: Synechocystis hypothetical protein s1r2144
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A;Molecule type: DNA
A;Residues: 1-274 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                  C;Accession: AI2836 J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, IR;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, IR;Wood, D.W.; Setubal, J.C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
                                                                                                                                                       A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; PMID:11743193
A;Accession: AI3836
A;Status: preliminary
A;Status: preliminary
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: lyc
                                                                                                                                                                                                                                                                                          A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                 Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
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                                                                               A;Residues: 1-283 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43111.1; PID:g17740583; GSPDB:GN00186
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es 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
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30.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.1%; Score 60; DB 2; Length 274; 26.2%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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A; Map position: circular chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Gold A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C;Accession: C97614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical 32.0K protein in fbaB-thiD intergenic region [imported] - Agrobacterium C; Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-354 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R. Rucleic Acids Res. 23, 2105-2119, 1995
Rucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from A;Reference number: S56314; MUID:95334362; PMID:7610040
A;Accession: S56421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probable hexulose-6-phosphate synthase (EC 4.1.2.-) [similarity] - Escherichia coli (N.Alternate names; hypothetical protein o216
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                                                                                                                                                                                                      A;Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97092.1; PID:g537037
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 01-Mar-2002 C; Accession: S56421; G65230
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                          A;Cross-references: GB:AE000491; GB:U00096; NID:g2367357; PIDN:AAC77153.1; PID:g17906
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-216 <BLAT>
                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Superfamily: hypothetical protein HI1024
C;Keywords: aldehyde-lyase; carbon-carbon lyase
                         A; Gene: yjfV
C; Superfamily: hypothetical
                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 HEVHGIDVSKWNGDVDWQTVRKSGVSFVFIKATEGSDRIDPKFGDHWRSA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HEAHKTSLSSWKHDQDWANV--SNMTF----SNGKLRVK---GIYYRNA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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32.0%;
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32.0%;
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Pred. No.
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                                                                                                                                   C;Superfamily: hypothetical protein HI1024
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A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-216 <STO>
                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                      A; Accession:
                                                                                                                                                                                                                                                                                                                                 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayheviller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
                                                                                                                                                                                                                                                                                                                                                                                               C: Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                           probable hexulose-6-phosphate synthase sgaH [imported] – Escherichia coli (strain O157:H
C;Species: Escherichia coli
                                                                             Query Match 16.0%; Score 59.5; Best Local Similarity 23.6%; Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.; Han, C.G. A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gend A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                        Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7 Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:BA000007; PIDN:BAB38595.1; PID:g13364649; GSPDB:GN00154
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A; Residues: 1-216 <HAY>
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C:Species: Escherichia coli
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     6 TSLSSWKHDODW--ANVSNMTESNGK-LRVKGTYYRNADICSRHRVT-----SAGLT 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 TGYWTWEQAQQWRDAGIQQVVYHRSRDAQAAGVAWGEADITAIKRLSDMGFKVTVTGGLA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 LQDLQLWCNLRI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 TSLSSWKHDQDW--ANVSNMTFSNGK-LRVKGIYYRNADICSRHRVT-----SAGLT 54
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23.6%; Pred. No. 12;
vative 16; Mismatches
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23.6%; Pred. No. 12;
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RESULT 15
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A:Gene: BH2678
C:Superfamily: succinyl-diaminopimelate desuccinylase
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                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-427 <STO>
                                                                                                                                                                                                                                                                                                                                               R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 17-May-2002
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                                                                                                                                                    Matches
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                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;48,212,268/Binding site: iron (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Leskiw, B.K.; Aharonowitz, Y.; Mevarech, M.; Wolfe, S.; Vining, L.C.; Westlake, D.W. Gene 62, 187-196, 1988
A;Title: Cloning and nucleotide sequence determination of the isopenicillin N synthet
A;Reference number: A29894; MUID:88212175; PMID:3130293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-329 <LES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isopenicillin N synthase (EC 1.14.11.-) [similarity] - Streptomyces clavuligerus C;Species: Streptomyces clavuligerus C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 26-May-2000
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419 YEWCHLR 425
                                             361 EEVKTSMSQTVTDGGWLAEAGIPTLLFGPGKLEDAHSVNEELEIAELVQYTKTLLTF--I 418
                                       59 QLWCNLR 65
                                                                                 2 EAHKTSLSSWKHDQDW----ANVSNWTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQDL 58
                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GTPMHEVNLW 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 GLTLQDLQLW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 NEFHGAMTDQEKHDLAIHAYNDDNPHVRNGYYKAVPGRKAVESFCYLNPDFGEDHPMIAA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HEAHKTSLSSWKHD------ODWANVSNMTFS--NGKLRVKGIYYRNADICSRHRVTSA 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 TGYWTWEQAQOWRDAGIQQVVYHRSRDAQAAGVAWGEADITAIKRLSDMGFKVTVTGGLA 173
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                                                                                                                                                              Similarity
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                                                                                                                                          Conservative
                                                                                                 16.0%;
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                                                                                                                                                            DB 2; Length 427;
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T15023
hypothetical protein Y1108 - Yersinia pestis plasmid pMT1
C;Species: Yersinia pestis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
C;Accession: T15023; T14697
R;Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIM5 plasmid A;Reference number: Z18268; MUID:99043898; PMID:9826348
A;Accession: T15023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AF074611; NID:g3883003; PID:g3883106; PIDN:AAC82766.1
R;Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Carrano, submitted to the EMBL Data Library, March 1998
A;Description: Structural organization of virulence determinants in three Yersinia pesti A;Reference number: Z18168
A;Accession: T14697
                                                                                                                                                                                                                                                                                                                                                       A;Gene: Y1108
A;Genome: plasmid pMT1
C;Superfamily: Yersinia pestis plasmid pMT1 hypothetical protein Y1108
Search completed: December 8, 2002, 19:34:47 Job time : 26.8129 secs
                                                                                                                       В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AF053947; NID:g2996286; PID:g2996333; PIDN:AAC13213.1 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-187 <HUP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-187 <LIN>
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                       124 DWADVANWLEANGRLK----ENAELAHNARVLS 152
                                                                                                                                                          16 DWANVSNMTFSNGKLRVKGIYYRNADICSRHRVTS 50
                                                                                                                                                                                                                                               Conservative
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Pred. No. 12;
7; Mismatches 9; Indels
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OM protein - protein search, using sw model
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Perfect score:
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Maximum DB seq length: 200000000
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No.
pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                 Score
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55.55
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Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                    Match
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Listing first 45 summaries
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46.1
46.1
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Backfiles1.pep:*
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   US-08-996-139-13
US-08-995-659-13
US-09-215-649A-13
US-09-052-521C-4
US-09-577-780-13
US-08-995-659-11
US-08-995-659-11
US-08-995-659-11
US-08-98-362-2
US-09-052-521C-3
US-09-052-521C-3
US-09-052-521C-34
US-08-594-031-102
US-08-594-031-102
US-08-13-231-5
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US-08-13-231-6
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US-08-13-321-10
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US-08-13-321-10
US-08-13-321-10
US-08-594-031-100
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US-08-594-031-100
US-08-594-031-100
US-08-595-648-31-5
US-08-595-648-31-5
US-09-457-56-48-31-5
US-09-457-56-48-31-5
US-09-557-56-48-31-5
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US-09-557-56-48-31-5
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                                                                                                                                                                            Sequence 13, Appl
Sequence 13, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 34, Appl
Sequence 34, Appl
Sequence 100, App
Sequence 100, App
Sequence 102, Appl
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9, Appli
93, Appl
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139-13 13, Application US/08996139 13, Application US/08996139 0. 6017729 INFORMATION: CANT: Anderson, Dirk M. CANT: Galibert, Laurent OF INVENTION: Receptor Activator OF INVENTION: Receptor Activator R OF SEQUENCES: 19 SPONDENCE ADDRESS: INMUNEX CORPORATION, LAW RESSEE: Inmunex Corporation, Law RESSEE: 19 SPONDENCE ADDRESS: ITER READABLE FORM: JUSA 98101 JUSA 98101 JUSA 99117 JUSA	54 14.5 146 4 US-08-584-031-16 54 14.5 149 3 US-08-584-031-16 54 14.5 151 1 US-07-940-605A-1 54 14.5 151 1 US-08-690-096-3 54 14.5 261 1 US-08-184-022-8 54 14.5 261 1 US-08-184-922-4 54 14.5 261 1 US-08-431-055-4 54 14.5 261 2 US-08-490-096-1 54 14.5 261 2 US-08-491-099-1 54 14.5 261 2 US-08-491-099-1 54 14.5 261 2 US-08-491-77-338-54 54 14.5 261 2 US-08-89-77-338-54 54 14.5 261 3 US-08-89-77-18-54 54 14.5 261 3 US-08-799-819-1 54 14.5 261 4 US-08-770-974-1 54 14.5 261 4 US-08-770-974-1
of NF-kappaB Department ystem 7.5.5 Macintosh 6.0.1	Sequence 1, Appli Sequence 16, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 12, Appli

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US-09-215-649A-•13
                       RESULT 3
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US-08-995-659-13
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hatent No. 6242213
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INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
                                        179 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                        Local Similarity 60.0 es 36; Conservative
                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                          NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 51 Uni
CITY: Seattle
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                                                                                                                                                                                                      amino acid
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Maraskovsky, Eugene
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                                                                                                                                                                                                                                                                       (206)587-0430
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14 OCTOBER 1997
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                                                                                                                     47.78;
60.08;
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60.08;
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                                                                                               Score 178; DB 4; Length 317; pred. No. 2.6e-15; 5; Mismatches 17; Indels
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Pred. No. 2.6e-15;
5; Mismatches 17; Indels
                                                                                            2; Gaps
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; SOFTWARE:
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Patent No. 6316408
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
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US-09-052-521C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-215-649A-13
                                                                  FILE REFERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
                    PRIOR APPLICATION NUMBER: 08/6
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
                                                                                                                                          TITLE OF INVENTION: OSTEC
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6271349
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                           179 SHKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                Match 47.7%;
Local Similarity 60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                      36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Anderson, Dirk M.
         PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 2851-A
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FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
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                                                                                                                                                   Osteoprotegerin Binding Proteins and Receptors
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Pred. No. 2.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 317;
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US-09-052-521C-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-577-780-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
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                                                                                                                           US-09-577-780-13
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human
                                                               Matches
                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (206)587-043
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                 PRICATION NUMBER: 08/995,659
APPLICATION NUMBER: USSN 08/813,509
APPLICATION NUMBER: USSN 08/813,509
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 2852-A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Power Macintosh operating System 7.5.5 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/577,780 FILING DATE: 24-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                          LENGTH: 317 amino acids
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.7%;
                                                                                                                                                                                                                                                                         (206)587-0430
                                                                                    47.78;
60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 178; DB 4; Length 317; pred. No. 2.6e-15; Mismatches 17; Indels
                                                                      5; Mismatches
                                                                         Score 178; DB 4; pred. No. 2.6e-15; pred. No. 2.7;
                                                                                                      DB 4; Length 317;
                                                                             Indels
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                                                                                Gaps
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RESULT 6

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US-08-996-139-11
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                                                                                                                                                                  ; Sequence 11,
; Patent No. 62
; GENERAL INFC
                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-996-139-11
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                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION USER: US/08/996 120
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATTICIA Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE: 07 MARC
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 51 Un
CITY: Seattle
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                                                                                 APPLICANT: Anderson, Dirk M.
APPLICANT: Gallbert, Laurent
APPLICANT: Maraskovsky, Bugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                              156 SHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL 215
                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
STREET: J. STREET: Seattle
                                                                                                                                                                                                                                                                                                                                3 AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                ADDRESSEE: Immunex COLPOTACE
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98101
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                                                                                                                                                                                         1, Application US/08995659 6242213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunex Corporation, Law Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                  Immunex Corporation, Law Department
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                         46.1%; Score 172; DB 3; Length 294; 56.7%; Pred. No. 1.5e-14; ative 6; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USSN 08/813,509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USSN 08/772,330
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COUNTRY:

USA

98101

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US-09-215-649A-11

Sequence 11, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-995-659-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                      156 SHKYTLSSWYHDRGWAKISNWTLSNGKLRVNQDGEYYLYANICERHHETSGSVPTDYLQL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operatir
                                                                                                                                                                                                                                  APPLICANT: Anderson, Dirk M.
Gallbert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 23 DE
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          APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                            STATE: WA
                                                                                                                                                                                    CITY: Seattle
                                                                                                                                                                                           ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 294 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: Apple Operating System 7.5.5
Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                           USA
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56.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 172; DB 4; Length 294; Pred. No. 1.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2852-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Indels
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US-09-577-780-11
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REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application Patent No. 6419929
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                           APPLICATION NUMBER: 08/995,659
FILING DATE: CUNKNOWN
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
                                                                                                                                                                                                                                                                                  FILING DATE: 24 May-2000 CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 46.1%; Score 172; DB 4; Length 294; Local Similarity 56.7%; Pred. No. 1.5e-14; les 34; Conservative 6; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
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RESULT 10 US-08-842-842-7

Sequence 7, Application US/08842842
Patent NO. 5843678
GENERAL INFORMATION:
APPLICANT: BOYLE, William J.
APPLICANT: NVENTION: OSTEOPROTEGE

OSTEOPROTEGERIN BINDING PROTEINS

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:

ADDRESSEE:

STREET: 1840 Denavi

1840 Dehavilland Drive

Amgen Inc

California

US-08-842-842-7

MOLECULE TYPE: protein TOPOLOGY: lincal

INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids

316 amino acids

ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.

NAME: Winter, Robert B. REFERENCE/DOCKET NUMBER: CLASSIFICATION: 435 FILING DATE: APPLICATION NUMBER:

A-451

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

US/08/842,842

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY:

91230-1789

Query Match Matches

watch 46.1%; Score 172; DB 2; Length 316; Local Similarity 56.7%; Pred. No. 1.6e-14; Local 34; Conservative 6; Mismatches 18; Indels

2;

RESULT 11 US-08-989-362-2

Sequence 2, Application US/08989362
Patent No. 6242586
GENERAL INFORMATION:

APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
TITLE OF INVENTION: Reagents
TITLE OF INVENTION: Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

ADDRESSEE:

DNAX Research Institute

Matches Query Match

Local

34; Conservative

Similarity

46.18; 56.78;

Score 172; DB 4; Length 294; pred. No. 1.5e-14;

6.

Mismatches

18; Indels

2;

TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid LENGTH: 294 amino acids

156 SHKYTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL 215

3 AHKTSLSSWKHDQDWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60

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3 AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-052-521C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local &
                                                                                                                            US-09-052-521C-2
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 В
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                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09052521C patent No. 6316408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                        SEQ ID NO 2
                                                                                                                                                                                                                                                                FILE REFERENCE: A-451BIV
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR FILING DATE: 1997-06-23
                                                        Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Boyle, William J. TITLE OF INVENTION: Osteopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: DX TELECOMMUNICATION INFORMATION: TELEPHONE: (650)852-9196
                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,846
ETILING DATE: 13-DEC-1996
                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 08/6
PRIOR FILING DATE: 1997-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                             TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 SHKYTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL 237
                                                                                                                                                                       LENGTH: 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AHKTSLSSWKHDQDWANVSNMTESNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
178 SHKYTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL 237
                                                                             Local Similarity
                             3 AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Conservative
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amino acid
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                     Osteoprotegerin Binding Proteins and Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.1%; Score 172; DB 4;
56.7%; Pred. No. 1.6e-14;
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                                                                                      46.1%;
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                                                                        6; Mismatches
                                                                                      Score 172; DB 4; Length 316; pred. No. 1.6e-14;
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                                                                               18; Indels
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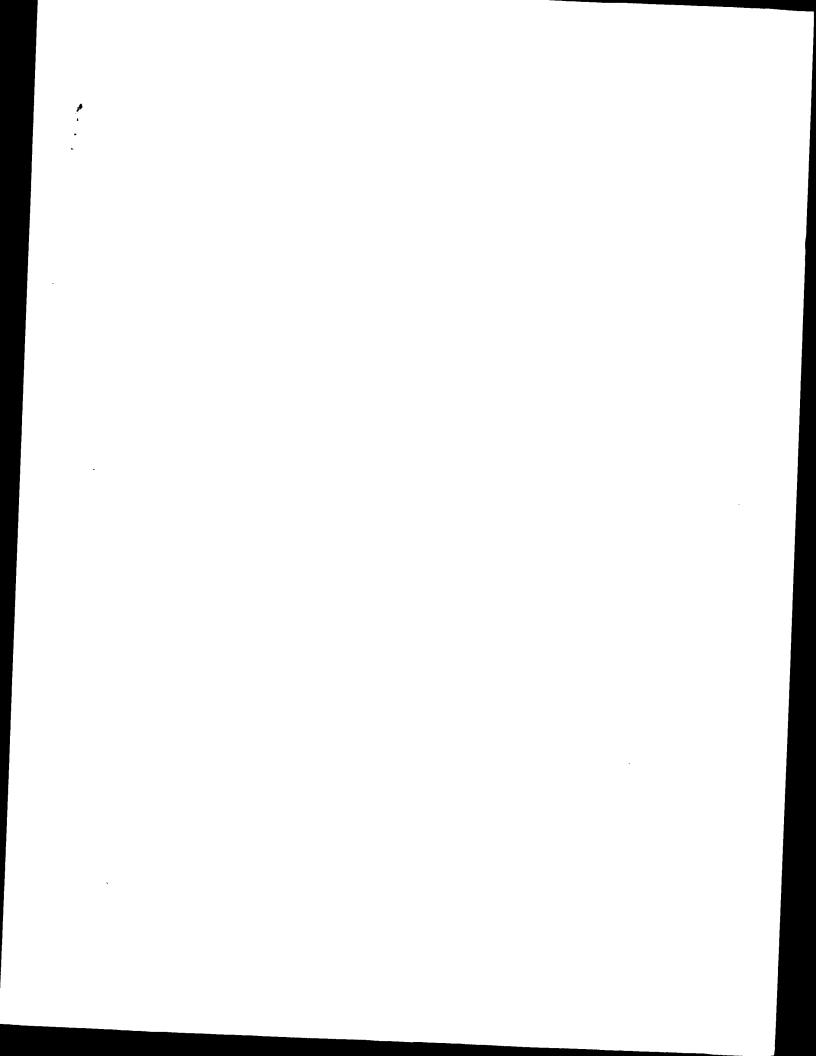
RESULT 13

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US-09-052-521C-34

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US-08-594-031-100
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                                                          INFORMATION FOR SEQ ID NO: 100:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5783182
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 100,
                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
SEQ ID NO 34
                                                                                                                                                                            FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR TOATTON NUMBER: 60/006,838
                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34, Application US/09052521C Patent No. 6316408
STRANDEDNESS:
                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-
                                                                                                                                  NAME: Remenick, James
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                          COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match
Local Similarity 57.9%; Score 72; DB 4; Length 28;
hes 11; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 SHKVTLSSWYHDRGWAKIS 27
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                    amino acid
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                               376 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5783182 US/08594031
                                                                                                                                                                                                                                                                                                                                                                                                                       E: BAKER & BOTTS, L.L.P.
1299 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                           IBM Compatible
SYSTEM: DOS
    single
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                                                                                                                                             36,902
                                                                                                                                0A146-0110
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US-08-594-031-102
    Query Match
16.9%; Score 63; DB 1; Length 376;
Best Local Similarity 22.1%; Pred. No. 3.1;
Matches 17; Conservative 16; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-594-031-102
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                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-594-031-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 102, Application US/08594031 Patent No. 5783182
                                                                                                                   MOLECULE TYPE: PO
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                         ORIGINAL SOURCE:
                                                                                                            FRAGMENT TYPE:
                                                                                                                                                                                                                                                             NAME: NEW TELEPHONE: 36,902
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/00
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                            TELEPHONE: 202-639-7890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: THOMPSON, TIMOTHY C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 11near
MOLECULE TYPE: pep
                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20004-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 YGHATTVGVNMTDVMVW 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 HDSHNYSTNYKWSGDNTGVSTNHTVNHTYVNGTSNTVKAAAGCRSKTSGAGDNSRDNCNR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 H-RVTSAGLTLQDLQLW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HEAHKTSLS-SWKHDQDWANVS---NMTFSNG-----KLRVKGIYYRNADICSR 45
                                                                                                                                                                                      amino acid
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1299 Pennsylvania Avenue, N.W.
                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
                                                                                                   N-terminal
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                                                                                                                                               peptide
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                                                                                                                                                                                                                                                                                                                                                                   60/006,838
                                                                                                                                                                                                                                                                                              0A146-0110
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Indels 16; Gaps
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OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
                                                                                                                                         Result
                                                                                                                                   NO.
                                                                                                                                                                       pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
5
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                                                                                                                                                                                                                                                                                                                                                                                                                                   671580 seqs, 206047115 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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                                                                                                                                     Match Length DB
                                                                                                                                              Query
                                                               14.8
14.8
14.8
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15.2
15.1
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sp_mammal:*
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sp_rvirus:*
sp_bacteriap:*
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491
491
1000
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296
307
478
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                                                   043651
096856
098031
09TT17
09TT17
                                                                                                           Q9DDZ5
Q88282
Q97BJ7
                                     Q94C88
     Q9NBK9
                    Q9FT49
                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (without alignments)
313.111 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                              671580
                                                                                                       Q9ddz5 brachydanio
Q88282 snakehead r
Q97bj7 thermoplasm
Q9fga8 arabidopsis
                   O9hc88 homo sapien
O9y6m7 homo sapien
O9x2g7 thermotoga
O9ft49 arabidopsis
Q71146 human immun
                                                                                        043651
Q96b56
                                                                                                                                              Description
                                                                         Q9bq31
Q9tt17
                                                           Q9uib9 homo sapien
060350 homo sapien
           Q9nbk9
                                                                       nomo sapien
7 oryctolagus
                                                                                                  homo sapien
                                                                                          homo sapien
             drosophila
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66.5
65.5
65.5
64.5
64.5
64.5
                                                                      63.5
63.5
63.5
63.5
63.5
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14.3
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286
212
131
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364
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621
237
276
                                     427
1485
156
262
267
297
561
813
287
287
287
246
246
246
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16
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                                                                                                                                        Q9G982
046867
049734
Q8RFS0
                                331086
                                                                                                                              0 Q9FWK6
Q9X6N2
                                                                                                                                                                        Q9VUN0
                                                                                            Q8SQ07
Q9FAC1
                                                  088008
800580
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                                                                                                        Q9NIW4
                                                                                                                    Q97L30
Q972X5
                                        Q9HDG3
                                                                                                              Q9K9G9
                                  Q9HEX9
                                                                    Q90WT9
                                                                          Q8YPE8
     Q9VJ73
                                             Q942B1
                       Q96Z32
                                                               Q8UIA0
                            Q8XTZ4
                Q96ZT5
                                                                                                      04974 arabidopsis
04974 arabidopsis
08rf80 fusobacteri
08rf80 fusobacteri
09rk6 cryza sativ
09730 clostridium
097130 clostridium
09725 sulfolobus
09899 bacillus ha
09niw4 caenorhabdi
09niw4 caenorhabdi
088907 saguinus oe
                                                                                                                                                           Q9g982 allomyces a O46867 ictalurus p
                                                                                                                                                                      Q9vun0 drosophila
Q9c6r2 arabidopsis
              Oghdy3 pneumocysti
Oghex9 pneumocysti
Oghex9 pneumocysti
Oghex12 ralstonia s
Oghex12 sulfolobus
Oghex15 sulfolobus
Oghm393 arabidopsis
                                                                                          Q9fac1 streptomyce
Q9vcj9 drosophila
                                                        Q8sq08 saimiri sci
Q8w109 chlamydomon
                                                                        Q8ype8 anabaena sp
Q913x9 pseudomonas
Q90wt9 gallus gall
        Q9vj73 drosophila
                                                                   Q8uia0 agrobacteri
                                                  Q942bl oryza sativ
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ALIGNMENTS

RESULT 1 Q9DDZ5 The property of a TNF receptor and two TNF receptor in the fish ovary. ";

RT ligands in the fish ovary. ";

RT LComp. Blochem. Physiol. B, Comp. Blochem. 129:475-481(2001).

DR HSSP, P50591; 1D0G.

DR HSSP, P50591; 1D0G.

R FINE, 2DB GEBUE-010801-1; tnfsf101.

DR HSSP, P50591; TNG. TNF_abc.

DR InterPro; IPR000478; TNF_family.

R InterPro; IPR000478; TNF_family.

R Ffam; PF00729; TNF; 1.

DR PAST; SM00207; TNF; 1.

SMART; SM00207; TNF; 1.

PR SMART; P50039; TNF_2; 1.

SMART; P5003049; TNF_2; 1.

SMART; P5003049; TNF_2; 1.

SR SMOURCE 214 AA; 24093 MW; 98C002474FF691AA CRC64; δõ Query Match Best Local S Matches Brachydanio rerio (Zebrafish) (Zebra danio). Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Cypriniformes; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Cyprinidae; Danio. NCBI_TaxID=7955; 01-MAR-2001 (TIEMBLIEL. 16, Created)
01-MAR-2001 (TIEMBLIEL. 16, Last sequence update)
01-MAR-2002 (TIEMBLIEL. 20, Last annotation update) Q9DDZ5 SEQUENCE FROM N.A. Bobe J., Goetz F.W.; Local Similarity es 15; Conserv |:: : : | : |:: ||: ||:|| | | | | : |: 76 HQSCRHPVHTWANKSFGAHLYNMTLTNGRLRVPQDGRYYLYSQVYFRY 123 20 HEAHKTSLSSWKHDODWANVSNMTFSNGKLRV--KGIVYRNADICSRH 65 PRELIMINARY; 15.2%; Score 69; DB 13; Length 23 ilarity 31.2%; Pred. NO. 2.9; Conservative 13; Mismatches 18; Indels PRT; 214 AA. DB 13; Length 214;

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A Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S., A Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S., A Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M., Yamamoto Y., Aramaki H., Makino K., Suzuki M., Yamamoto Y., Aramaki H., Makino K., Suzuki M., Yamamoto T., Yamamoto Y., Aramaki H., Makino K., Suzuki M., Kawamoto Y., Aramaki H., Makino K., Suzuki M., Yamaki H., Makino K., Suzuki M., Kawamoto Y., Aramaki H., Makino K., Aramaki H., Makino K., Suzuki M., Yamaki M., Yamaki H., Makino K., Suzuki M., Yamaki M., Yam
                                          Matches
                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
Q97BJ7
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Q88282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                           STRAIN-GSS1 / DSM 4299 / JCM 9571;
MEDLINE-20570466; PubMed-11121031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2001 (TrEMBLrel 18, Created)
01-OCT-2001 (TrEMBLrel 18, Last sequence update)
01-MAR-2002 (TrEMBLrel 20, Last annotation update)
TY0458 OR TYG0449104
                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermoplasma volcanium.
Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=50339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q97вJ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                    hermoplasmataceae; Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532 TKTLKTGVTWTTAVVKIDLQQWVDI 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hart D., Frerichs G.N., Rambaut A., Ronalds R.J., Onions D.E.; Evidence for a new retrovirus genus of piscine origin.", Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U26458; AAC54858.1; SEQUENCE 1130 AA; 128317 MM; B6A4F8095E4F0D3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             476 SSGNSWKAEIDKIRKOKW-----OKCYFSGKLRIKGTDYEBIDTCPKPLIGPLSGFIPTGV 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hart D., Frerichs G.N., Rambaut A., Onions D.E., "Complete nucleotide sequence and transcriptional analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 GLTLQ------BLQLWCNL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-96211493; PubMed-8648695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 TSLSSWKHD-----QDWANVSNWTFSNGKLRVKGIYYRNADICSRHRV-----TSA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=40270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Snakehead retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TremBirel
01-NOV-1996 (TremBirel
01-DEC-2001 (TremBirel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Envelope protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q88282;
Q88282;
                     23: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70:3606-3616(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Retroid viruses; Retroviridae; Epsilonretrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
           15.1%; Score 68.5;
27.1%; Pred. No. 2;
ative 17; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.2%; Score 69; DB 15; Length 1130; 25.9%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Mismatches
              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1130 AA.
                                          DB 17; Length 1171;
32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Indels
13;
                                                                                                                                                                                                                                                                           Kawamoto
Gaps
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RESULT 5
        Am. J. Physiol. 277:C412-C424(1999).
EMBL; AF043472; AAC13164.1;
InterPro; IPR0002210; BTB_POZ.
InterPro; IPR001522; K+Channel_pore.
InterPro; IPR003968; Kv_Channel.
                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                          Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
                                                                    "Electrically silent potassium channel subunits from human lens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                        MEDLINE=99413882; PubMed=10484328; Shepard A.R., Rae J.L.;
                                                                                                                                     TISSUE=LENS EPITHELIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                γ
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last amoutation updat
                                                                                                                                                                                                                    Shab-related delayed-rectifier K+ channel alpha subunit.
                                                                                                                                                                                                                                                                                             043651;
                                                                                                                                                                                                                                                                                                       043651
                                                                                                                                                                                                                                                                                                                                                            159 TLOMEQL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
SEQUENCE 187 AA; 20056 MW; 305781D3A0738AEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    102 HDAYVGILASLKSALLELKDSPDTANYDVMVSGDDTRRVKGLVEKNTDTASK---TLMEM 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Similarity to pollen-specific protein Bnml.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9FGA8;
                                                                                                                                                                                                                                                                                                                                                                                                           20 HEAH-----KTSLSSWKHDQDWANVSNMTFSNGKLRVKGIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         942 YPKNLTSLVITINGLRLRCEADFIN 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        885 LWEPALGHYVLNFTYVTKTSNWINNTLYANLSNYAPAIYLKISNRDL--NGSYYLHI-LA 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 SRHRVTSAGLTLQDLQLWCNLRIIH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 LLIPSISHE----AHKTSLSSWKHDQDWANVSN-----MTFSNGKLRVKGIYYRNADIC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassicales, Brassicaceae, Arabidopsis.
K_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.98; 32.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68; DB
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                       491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               _DB 10; Length 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  core eudicots; Rosidae;
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InterPro; IPR000636; M+channel_nlg. InterPro; IPR003131; K_tetra

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Вр
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 14.8%; Score 67.5; DB 4; Length 491; Best Local Similarity 22.0%; Pred. No. 12;
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                                                                                                                                                                                                            В
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                                                                                              Q9BQ3
BEBBBBBB
                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00520; ion_trans; 1.
pfam; PF02214; K_tetra; 1.
pRINTS; PR00169; KCHANNEL.
PRINTS; PR01494; KV9CHANNEL.
PRINTS; PR01491; KVCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00225; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ionic channer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
potassium voltage-gated channel, delayed-rectifier, subfamily S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q96B56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 -----DTHPVTLAGKLIASTCIICGILVV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 LLFLSVGISIFSVLIYSVEKDDHTSSLTSIPICWW-----WATISMTTVGYG------ 374
                                                                                                                                                                                                                                                                                                                                         Pfam; PF00520; Pfam; PF02214;
                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC015947; AAH15947.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-SKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                      InterPro;
          O9BQ31;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
unknown (Protein for MGC:4213) (Potassium voltage-gated channel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 YRNADICSRHRVTSAGLTLQDLQLWCNLRII 86
                                                                                 Q9BQ31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAILTLSLQLILLLIPSISHEAHKTSLSS-----WKHDQDWANVSNMTFSNGKLRVKGIY 55
delayed-rectifier,
                                                                                                                                                    375 -----DTHPVTLAGKLIASTCIICGILVV 398
                                                                                                                                                                                                            328 LLFLSVGISIFSVLIYSVEKDDHTSSLTSIPICWW-----WATISMTTVGYG------ 374
                                                                                                                                                                                56 YRNADICSRHRVTSAGLTLQDLQLWCNLRII 86
                                                                                                                                                                                                                                      1 MAILTLSLQLILLIPSISHEAHKTSLSS-----WKHDQDWANVSNMTFSNGKLRVKGIY 55
                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      491 AA;
                                                                                                                                                                                                                                                                                                                                                                    ipR001622; K+channel_pore.
ipR003131; K_tetra.
ipR000636; M+channel_nlg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                              491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                        Conservative
                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                          ion_trans; 1.
                                                                                                                                                                                                                                                                                                                                            K_tetra;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55970 MW; FFF12CA3CDA50185 CRC64;
                                                                                                                                                                                                                                                                                                                                tra; 1.
56047 MW;
    subfamily S, member 3).
                                                                                                                                                                                                                                                                                    14.8%; Score 67.5;
22.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Mismatches 30; Indels
                                                                                                                                                                                                                                                                         16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                185D80646109C629 CRC64;
                                                                                        PRT;
                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491 AA
                                                                                           491 AA
                                                                                                                                                                                                                                                                                                      DB 4; Length 491;
                                                                                                                                                                                                                                                                            30; Indels
                                                                                                                                                                                                                                                                               25;
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DE GN OOC OC OC OC RN RP RC RA RL DR RL DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BBBBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0169; KCHANNEL.
PRINTS; PRO1492; KV9CHANNEL.
PRINTS; PRO1494; KV9CHANNEL.
PRINTS; PRO1491; KV9CHANNEL.
PRINTS; PRO1495; SHABCHANNEL.
PRINTS; PRO1495; SHAWCHANNEL.
PRINTS; PRO1498; SHAWCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                      InterPro; IPR000210; BrB_POZ.
InterPro; IPR001622; K-channel_pore.
InterPro; IPR003971; Kv9_channel.
InterPro; IPR003986; Kv_channel.
InterPro; IPR003991; K_channel.
InterPro; IPR003991; K_channel.
InterPro; IPR003131; K_tetra.
InterPro; IPR003131; K_tetra.
InterPro; IPR003131; K_tetra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00520; ion_trans; 1. Pfam; PF02214; K_tetra; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR003091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9TT17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Ciditaca, Veterrari, Eukaryota; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Voltage-gated delayed-rectifier potassium channel Kv9.3
                                                                                                                                                                                                                                                                  Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                   STRAIN-NEW ZEALAND WHITE; TISSUE-CORNEA ENDOTHELIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCNS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 -----DTHPVTLAGKLIASTCIICGILVV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 LLFLSVGISIFSVLIYSVEKDDHTSSLTSIPICWW-----WATISMTTVGYG-----
                                                                                                                                                                                                                                     EMBL; AF209723; AAF22833.1;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9986;
     Pfam; PF02214; K_tetra; l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 YRNADICSRHRVTSAGLTLQDLQLWCNLRII 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAILTLSLQLILLLIPSISHEAHKTSLSS-----WKHDQDWANVSNMTFSNGKLRVKGIY 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocal
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CE 491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003973; Shab_channel.
IPR003974; Shaw_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR003969;
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IPR001622; K+channel_pore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR003971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BTB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K_channel.
K_tetra
M+channel_nlg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55984 MW; A5F12BF077A50DAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kv_channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kv6_channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.8%; Score 67.5;
22.0%; Pred. No. 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kv9_channel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          491 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                        Matches
Homo sapiens (Human).
Eukaryota; Metazoą; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                    01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                             Sodium bicarbonate cotransporter2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                060350;
                                                                                                                                              060350
                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P02730, 1BNX.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotransp.
Pfam; PP00955; HC03_cotransp; 1
PRINTS; PR01231; HC03_TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGRO0834; ae; SEQUENCE 1000 AA; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of a HCO3 transporter, NT2-NBC, from human brain, similar to both the Anion exchangers (AEs) and the Na/Bicarbonate Cotransporters
                                                                                                                                                                                                                   606 YIPDVLFWC 614
                                                                                                                                                                                                                                                             558 PNPSNE----TLAQWKKDNITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GP 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF053755; AAF21720.1; -
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                          73 TLQDLQLWC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bicarbonate transporter.
                                                                                                                                                                                                                                                                                        16 PSTSHEAHKTSLSSWKHDQDWA-NVS--NMTFSNGKLRVKGIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Comero M.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ω9UIB9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9UIB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS: PRO0169: KCHANNEL.
PRINTS: PR01494: KV9CHANNEL.
PRINTS: PR01491: KVCHANNEL.
SMART: SM00225; BTB; 1.
IOnic Channel.
                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 -----DTHPVTLAGKLIASTCIICGILVV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 LLFLSVGISIFSVLIYSVEKDDHTSSLTSIPICWW-----WATISMTTVGYG------ 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 YRNADICSRHRVTSAGLTLQDLQLWCNLRII 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAILTLSLQLILLLIPSISHEAHKTSLSS-----WKHDQDWANVSNMTFSNGKLRVKGTY 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491 AA; 55941 MW; 2EE396E0889D6F77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                         14.8%; Score 67.5; DB 4; 31.9%; Pred. No. 27; ative 14; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                              112501 MW; 93FAA40A3141F8F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.8%; Score 67.5; DB 6; Length 491; 22.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Mismatches
                                                                                                                                        PRT;
                                                                                                                                      1018 AA
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                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 1000;
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                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                        InterPro: IPR001717; Anion_exchange.
InterPro: IPR001717; Anion_exchange.
InterPro: IPR003020; HC03_cotransp.
Pram: PF00955; HC03_cotransp: 1.
PRINTS; PR01231; HC03TRNSPORT.
TIGRFAMS; TIGR00834; ae; 1.
SEQUENCE 1090 AA; 123080 MW; 541839CC9B565896 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9HC88;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Sodium bicarbonate cotransporter 2b.
696 YIPDVLFWC 704
                                                                                           648 PNPSNE----TLAQWKKDNITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GP 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF089726; AAG16773.1; -- HSSP; P02730; IBNX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pushkin A., Abuladze N., Newman D., Hwang J., Kurtz I.; "Homo sapiens sodium bicarbonate cotransporter 2b mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-KIDNEY
                                                                                                                                                      16 PSISHEAHKTSLSSWKHDQDWA-NVS--NMTFSNGKLRVKGIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9нс88
                                                           73 TLQDLQLWC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotransp.
Pfam; PF00955; HC03_cotransp; 1.
PRINTS; PR01231; HC03FRNSPORT.
TIGRFAMS; TIGR00834; ae; 1.
TIGRFAMS; TIGR00834; ae; 1.
SEQUENCE 1018 AA; 114204 MW; A37799D93AlE30BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 0:0-0(1998).
EMBL; AB012130; BAA25898.1; -.
ESSP; P02730; IBNX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               606 YIPDVLFWC 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           558 PNPSNE----TLAQWKKDNITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GP 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ishibashi K., Sasaki S., Marumo F.;
"Molecular cloning of a new sodium bicarbonate cotransporter cDNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-RETINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 PSISHEAHKTSLSSWKHDQDWA-NVS--NMTFSNGKLRVKGIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 TLQDLQLWC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                     14.8%; Score 67.5; DB 4; Length 1090;
31.9%; Pred. No. 30;
tive 14; Mismatches 18; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.8%; Score 67.5; 31.9%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
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                                                                                                                                                                                                                           15;
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RESULT 12
Q9Y6M7
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Q9X2G7
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Matches
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Sodium bicarbonate cotransporter 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0946м7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99278433; PubMed=10347222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE 794,043, No. Tee I., Newman D., Hwang J., Kurtz I., pushkin A., Abuladze N., Lee I., Newman D., Hwang J., Kurtz I., pushkin A., tissue distribution, genomic organization, and function "Cloning, tissue distribution, genomic organization, and function "Cloning, tissue distribution, genomic organization, and function of NBC3, a new member of the sodium bicarbonate characterization of NBC3, a new member of the sodium bicarbonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF047033; AAD38322.1; HSSP; P02730; 1BNX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cotransporter family.";
J. Biol. Chem. 274:16569-16575(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning, tissue distribution, genomic org
characterization of NBC3, a new member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prim; PF00955; HCO3_cotransp; 1.
PRIMYS; PR01231; HCO3TRNSPORT.
TIGREAMS; TIGR00834; ae; 1.
SEQUENCE 1214 AA; 136042 MW; EF203500B5BF5267 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotransp.
                                                    Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Heidelberg J., Sutton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Frischmann R.D., Eisen J.A., White O.,
Heidelberg J., Smith H.O., Venter J.C., Fraser C.M.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
Byjdence for lateral gene transfer between Archaea and Bacteria from
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).

Nature 399:323-329(1999).

EMBL; AE001822; AAD36914.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
Hypothetical protein TM1852.
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed-10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        820 YIPDVLFWC 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 PSISHEAHKTSLSSWKHDQDWA-NVS--NMTFSNGKLRVKGIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2336;
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   Hypothetical protein; Complete proteome.
SEQUENCE 296 AA; 34197 MW; 11B3960CA5C3D2C6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and functional
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Hypothetical 34.9 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress). Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; eudicotyledons; Core eudicots; Rosid Spermatophyta; Magnoliophyta; eudicotyledons; Arabidopsis. eurosids II. Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 BEDWEKFGGVPNVVFSDAMIEYNGYYYVYYGAADNC----IALATIPVEKVMKWC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alcaraz J.P., Clabault G., Cottet A., Mache R., Mewes H.W.,
Lemoke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing project; submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases EMBL, AL132972; CAC07924.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 DODW---ANVSNMTFSNGKLRVKG---TYYRNADICSRHRVTSAGLTLODLOLWC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     Q71146
Q71146;
                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      149 HDEYKVLSFIWRHNKEWKVRSEHHVLVLGARTSWKKTQCHIHHLPYSQG-ITINGVLYYG 207
                                                                                                                                                                                                                                                                                                                                                                               208
                                                                                                                                                                                Viruses; Retroid viruses;
                                                                                                                                                                                               Human immunodeficiency virus type 1
                                                                                                                                                                                                                       Envelope glycoprotein gp120 (Fragment)
                                                                                                                                                                 NCBI_TaxID=11676;
                                                          Quinones-Mateu M.E., Dopazo J., Este J.A., Rota T.R., Domingo E., "Molecular characterization of human immunodeficiency virus type isolates from Venezuela.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 HEAHKTSLSSWKHDQDW----------ANVSNMTFSNGKLRVKGIYYRN 58
                                                                                                      MEDLINE=96093896; PubMed=7576917;
                                                                                                                                                                                                                                                                                                                                                                                                            59
   STRAIN-VE2;
                SEQUENCE FROM N.A.
                                               AIDS Res.
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             AWTDDKCVLMSFDLTSEDVGVW 229
                                                                                                                                                                                                                                                                                                                                                                                                            ADICSRHRVTSAGLTLQDLQLW 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al protein 307 AA;
                                               Hum. Retroviruses 11:605-616(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.7%; Score 67; DB ... 27.3%; Pred. No. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34863 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.7%; Score 67; DB
18.3%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Mismatches
                                                                                                                                                                                        Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DC8746CB47D8F92E CRC64;
                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307
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                                                                                                                                                                                                                                                                                                                    478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 307;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       December 8, 2002, 17:26:33; Search time 41.2387 Seconds (without alignments) graph of the control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-880-457-4_COPY_20_87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEAHKTSLSSWKHDQDWANV......TSAGLTLQDLQLWCNLRIIH 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum Match 100%
Listing first 45 summaries
A_Geneseq_101002:*

/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1980.DAT:*

/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1981.DAT:*

/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1981.DAT:*

/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1983.DAT:*

/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1983.DAT:*

/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1985.DAT:*

/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1987.DAT:*

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/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1987.DAT:*

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/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1997.DAT:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10087554682	Result
358 178 178 178 178 178 178 178 178 178	Score
96.0 47.7 47.7 47.7 47.7 47.7 47.7 47.7 47	Query Match Length DB
95 152 160 244 244 246 246 317 317 317	ength [
23 22 21 23 23 19 19 19 19)B ID
AAU83632 AAB67248 AAB68273 AAU86148 AAU78286 AAU78286 AAW83020 AAW83195 AAW83195 AAW83918 AAW69957 AAW68293	(D
Human RANKL. Homo Amino acid sequenc Amino acid sequenc Human pRO206 polyp Human TRANCE prote Osteoclastogenesis Human osteoprotege Osteoclastogenesis NF-kB receptor act	Description Human PRO protein,

RESUL AAU83 AAU83 XX XX XX XX AC	113 113 114 115 116 117 117 118 119 119 119 119 119 119 119 119 119
ALIGNMENTS AAJB3632 standard; Protein; 95 AA. AAJB3632; 08-MAY-2002 (first entry) 08-MAY-2002 (first entry) Human PRO protein, Seq ID No 82. Human; secreted protein; PRO; tumour; liver tumour; breast cancer; prostate tumour; rectal tumour; liver tumour; cumour necrosis factor-alpha. Homo sapiens. WO200208288-A2. 31-JAN-2002. 29-JUL-2000; 2000US-219556P. 25-JUL-2000; 2000US-219556P. 25-JUL-2000; 2000US-220605P. 25-JUL-2000; 2000US-220605P. 25-JUL-2000; 2000US-220604P. 25-JUL-2000; 2000US-220638P. 25-JUL-2000; 2000US-220638P. 25-JUL-2000; 2000US-22063P. 26-JUL-2000; 2000US-22063P. 26-JUL-2000; 2000US-22063P. 28-JUL-2000; 2000US-22063P.	178 47.7 317 21 AAY84 178 47.7 317 22 AAE08 178 47.7 317 22 AAE08 178 47.7 317 22 AAE08 178 47.7 317 22 AAE019 178 47.7 317 22 AAE019 178 47.7 317 23 AAU78 179 46.9 318 22 AAAB3 170 46.1 160 21 AAY8 170 46.1 173 21 AAY8 170 46.1 173 21 AAY8 170 46.1 182 21 AAY8 170 46.1 294 19 AAW8 170 46.1 294 19 AAW8 170 46.1 294 22 AAE0 170 46.1 316 19 AAW 170 46.1 316 19 AAW 170 46.1 316 19 AAW 170 46.1 316 21 AAY8 170 46.1 316 21 AAY8 170 46.1 316 21 AAW 170 46.1 316 2

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                              CC encoding PRO polypeptides. The sequences of the 122 PRO polypuctides CC encoding PRO polypeptides. The sequences of the 122 PRO polypuctides CC encode human secreted proteins. The PRO nucleic acids, polypeptides, CC agonists and antagonists are useful for treating a PRO related disorder. CC concer, colon cancer, breast tumour, prostate tumour, rectal tumour or CC liver tumour. The PRO polypeptides are useful for stimulating the CC proliferation of, or gene expression, in pericyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, CC stimulating or inhibiting the proliferation of conditions in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AAU83592-AAU83713 represent human processis protein sequences of the invention.
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                               Matches
Homo sapiens.
           Human; Apo2 ligand: divalent metal ions; viral infection; cancer.
                                                             Human RANKL
                                                                               18-APR-2001 (first entry)
                                                                                                                               AAB67248 standard; protein; 152 AA.
                                                                                                                    AAB67248;
                                                                                                                                                                                                             80 WCNLRSV 86
                                                                                                                                                                                                                                        61 WCNLRII 67
                                                                                                                                                                                                                                         20 HEAHKTSLSSWKHDQDWANVSNWTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-AUG-2000; 2000WO-US23522.
24-AUG-2000; 2000WO-US23328.
15-SEP-2000; 2000WG-US20873.
10-NOV-2000; 2000WO-US30873.
28-NOV-2000; 2000WO-US30873.
01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US32678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Figure 82; 359pp; English.
                                                                                                                                                                                                                                                        1 HEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-172001/22.
                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABK33576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-2000;
                                                                                                                                                                                                                                                                                                                          65;
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desnoyers L,
C, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2000WO-US34956.
; 2001WO-US06520.
; 2001US-0854280.
; 2001WO-US17092.
                                                                                                                                                                                                                                                                                                                            96.0%;
97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerritsen ME, Goddard A, Godowski p
Smith V, Stephan JF, Watanabe CK,

    Mismatches

                                                                                                                                                                                                                                                                                                  Score 358; DB 23; Length 95; pred. No. 2.3e-39; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Godowski PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood WI;
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AAB08273
                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides comprising tumour necrosis factor ligand family proteins, useful for treating inflammatory and immune disorders, e.g.
                                               WPI; 2000-558217/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                     Boyle WJ, Hsu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                         11-FEB-2000; 2000WO-US03653.
                                                                                          (AMGE-) AMGEN INC.
                                                                                                                12-FEB-1999;
18-NOV-1999;
                                                                                                                                                                    17-AUG-2000.
                                                                                                                                                                                       WO200047740-A2.
                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                    AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease; type II transmembrane protein; B cell stimulatory factor;
                                                                                                                                                                                                                                                                         Amino acid sequence of a human TNF ligand QPGL.
                                                                                                                                                                                                                                                                                                  04-DEC-2000 (first entry)
                                                                                                                                                                                                                         lupus and graft versus host disease.
                                                                                                                                                                                                                                                                                                                               AAB08273;
                                                                                                                                                                                                                                                                                                                                          AAB08273 standard; Protein; 160 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a formulation comprising Apo-2 ligand and divalent metal ions. Apo-2 ligand and the formulation of the treating cancers and viral infections. Addition of divalent metal ions for making Apo-2 ligand and formulations containing Apo-2 ligand results in increased yield and stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 3; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of divalent metal ions for making Apo-2 ligand and in formulations containing Apo-2 ligand for increasing yield and stability of ligand trimers, useful for therapeutic applications -
                                                                                                                                                                                                                                                                                                                                                                                17 SHKYSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-123012/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O'Connell M,
                                                                                                                                                                                                                                                                                                                                                                                              Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Loca1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2000; 2000WO-US17579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W0200100832-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 AA;
                                                                                                            99US-0166271.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                      9908-0119906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pai R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0141342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hymowitz S,
                                                                                                                                                                                                                                                                                                                                                                                                                           47.7%; Score 178; DB 22; Length 152; 60.0%; Pred. No. 2.2e-15; tive 5; Mismatches 17; Indels
                                                                                                                                                                                                                         immune disorder; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shahrokh z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kelley RF, Koumerokh Z, Simmons L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koumenis I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leung S;
                                                                                                                                                                                                                                                                                                                                                                                                                           2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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rheumatoid arthritis -

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AAAB08265-83 represent tumour necrosis factor (TNF) ligands. The specification describes an AGP-3 polypeptide, which is TNF ligand SC specification describes an AGP-3 polypeptide, which is TNF ligand Content and the second sec
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; Fig 9; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU86148 standard; Protein; 244 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU86148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disoinflammatory disorder; immune disorder; angiogenic disorder; inflammatory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO206 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200153486-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-1999;
11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AHKTSLSSWKHDODWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLODLOL 60
                                                                                                                                                                                                                                                                                                                                                       02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                          11-MAY-1999;
                                                                                                                                                                                                                                                                                                                22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                    22-JUN-1999;
                                                                                                                                                                                           01-SEP-1999
                                                                                                                                                                                                                   31-AUG-1999;
                                                                                                                                                                                                                                                                           26-JUL-1999;
                                                                                                                                                                                                                                                                                               20-JUL-1999;
                                                                                                                                                         30-NOV-1999
Marsters SA,
                                                        (GETH ) GENENTECH INC.
                   Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000WO-US03565.
                                                                                                     2000WO-US00219
        Pan J,
                                                                                                                                                                                                                                                                                                                                                                                   99US-133459P
                                                                                                                                                                                                                                                                                                                                                                                                  99US-123972P.
                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US05028.
                                                                                                                                                                                                                                           99US-149395P.
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                                                                                                                                                                                                        99WO-US20111
                                                                                                                                                                                                                          99US-
                                                                                                                                                               99WO-US28313.
                            Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.78;
                                                                                                                                                                                                                                151689P.
               Pitti RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 178; DB 21;
pred. No. 2.4e-15;
5; Mismatches 17;
                                Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                 Roy MA,
                                         Gurney AL,
                     Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          blastocoelic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                            Stone DM;
                                               Hillan KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, analogosists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastoccelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. AAU86128-AAU86162 represent the human PRO polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, anglogenic and immunologic disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABK40274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 61; Fig 42; 302pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the isolation of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU78286 standard; Protein; 244 AA
                                                                                                                                                                                                                                                                                                                                                                                       TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy; bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis; heumatoid arthritis; acromegaly; gigantism; exostosis; carilaginea; rheumatoid arthritis; acromegaly; gigantism; exostosis; chondrocyte; exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human TRANCE protein splice variant 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU78286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 SHKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; tumour necrosis factor-related activation induced cytokine;
                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                           cartilage growth; skeletal growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                WO200216551-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AHKTSLSSWKHDODWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLODLOL
                                                                                                                                                                                      (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT
                                                                                                                                                                                                                   18-AUG-2000; 2000US-226197P
                                                                                                                                                                                                                                                  20-AUG-2001; 2001WO-US26101.
                                                                                                                                                                                                                                                                                   28-FEB-2002
                                           Treating mammal having disorder characterised by abnormal cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor-related activation induced administering tumour necrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002-205567/26.
                                                                                                          N-PSDB; ABK12877
Disclosure; Fig 4; 55pp; English.
                              cytokine-modulating agent to mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                               2002-304119/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wood WI;
                                                                                                                                                          Odgren PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.7%;
                                                                                                                                                                Marks SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 178; DB 23;
Pred. No. 4.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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RESULT 6
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X S S S S S S S S S S S S S S S S S X &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a new method of treating a mammal CC having a disorder comprising insufficient or excessive cartilage or CC skeletal growth. The method of the invention involves administering to the mammal a tumour necrosis factor-related activation induced cytokine (TRANCE) modulating agent. The method is useful for treating a mammal CC having a disorder comprising insufficient or excessive cartilage or CC skeletal growth, where the disorder comprising insufficient cartilage or CC craniofacial skeletal discrepancies and bone or cartilage activation from traumatic injury, surgery, osteoarthritis or rheumatoid CC excessiving from traumatic injury, surgery, osteoarthritis or rheumatoid CC exostosis bursate and multiple osteoarthritis, and disorders comprising excessive cartilage or skeletal cc is useful for inhibiting chondrocyte differentiation. The present amino CC acid sequence represents the human TRANCE protein, splice variant 2, of the invention. TRANCE is a member of the tumour necrosis factor family
Example 28; Pages 119-120; 151pp; Japanese.
                                             Protein binding to osteoclastogenesis inhibitory factor - useful
                                         calcium metabolism
                                                                                                         WPI; 1998-594563/50.
                                                                                                                                                                                                                                       15-APR-1997;
09-JUN-1997;
12-AUG-1997;
                                                                                                                                 Nakagawa N, Shima N, Tai
Washida N, Yamaguchi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 36;
                                                                                                                                                                       Goto M,
                                                                                                                                                                                   (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                02-DEC-1997;
                                                                                                                                                                                                                                                                                                          15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                               WO9846644-A1
                                                                                                                                                                                                                                                                                                                                                                                                       Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM osteoclast; bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW83020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW83020 standard; Protein; 246 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 SHKYSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and acts directly on cartilage-producing cells (chondrocytes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADIGSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                 AAV69899
                                                                                                                                                  Higashio K,
N, Shima N,
                                      treatment and investigation of disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 AA;
                                                                                                                                                                                                                               97JP-0097808
97JP-0151434
97JP-0217897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                  97JP-0224803
                                                                                                                                                                                                                                                                          97JP-0332241.
                                                                                                                                                                                                                                                                                                    98WO-JP01728.
                                                                                                                                                   Kinosaki M, Kobayashi F,
                                                                                                                                             Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.78;
60.08;
                                                                                                                           Yano K, Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 178; DB 23;
Pred. No. 4.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                   of bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 244;
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AAW83195
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The present sequence is human osteoprotegerin (OPG) binding protein. Host cells transfected with vectors containing nucleic acid molecules encoding OPG binding protein are used to produce recombinant OPG binding protein is used in binding assays to determine osteoprotegrin (OG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful in immunoassays for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              555555555555555555555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents an osteoclastogenesis inhibitory factor (CCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone. CC absorption factors such as calcitriol or parathyroid hormone (PTH). CC absorption factor by separation and solubilisation of membrane proteins cC then affinity chromatography using OCIF. It exists in a full-sequence cC used for screening potential inhibitors and modifiers of its biological function and screening for receptors to OBM which mediate its function. CC These substances can then be used in the treatment of disorders of bone cC function and calcium metabolism. The antibodies can be used for assay commonents of drings.
                                                                                                                                     Claim 19; Fig 4; 47pp; English.
                                                                                                                                                                Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation
                                                                                                                                                                                                                                      N-PSDB; AAV70285
                                                                                                                                                                                                                                                                                                                                                        30-MAR-1998;
16-APR-1997;
                                                                                                                                                                                                                                                 WPI; 1998-594578/50.
                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                             23-ЈИМ-1997;
                                                                                                                                                                                                                                                                                                                                                                                                   15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09846751-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoprosis; osteoclast maturation; bone disease; metastasis; ODAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypercalcaemia; osteoclast differentiation and activation receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW83195 standard; Protein; 317 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW83195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 SHKYSLSSWYHDRGWAKISNWTESNGKLIVNQDGEYYLYANICERHHETSGDLATEYLQL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                    97US-0842842.
97US-0880855.
                                                                                                                                                                                                                                                                                                                                                                 98US-0052521.
                                                                                                                                                                                                                                                                                                                                                                                             98WO-US07584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.7%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 178; DB 19;
Pred. No. 4.2e-15;
5; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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AAW83018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences, e.g. screening for related sequences, also to produce requences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for antisense regulation of OpG binding protein expression. Modulators of antisense regulation of OpG binding protein protein, particularly soluble forms of OpG binding protein opG binding protein, particularly soluble forms of OpG binding protein or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis, or Ab, are used by arthritis or metastases, hypercalcaemia, Paget's bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, loosening of prostheses, optionally in combination with agents that promote bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection of OPG binding protein) and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding OPG binding protein can be used to detect OPG binding protein-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW83018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW83018 standard; Protein; 317 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-1997;
12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09846644-AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            osteoclast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1997;
15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-APR-1998;
The present sequence represents an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). By its isolated from stroma cells cultured in the presence of a bone obm is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins
                                                                                                                                                                                                                                                                                      Goto M, Higashio K, Kin
Nakagawa N, Shima N, Tak
Washida N, Yamaguchi K,
                                                                                                                                                                                                                                                                                                                                                              (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                   21-AUG-1997;
                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                protein binding to osteoclastogenesis inhibitory factor - useful
for, e.g. treatment and investigation of disorders of bone and
                                                                                                                               Claim 36; Pages 113-114; 151pp; Japanese.
                                                                                                                                                                  calcium metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AHKTSLSSWKHDQDWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cal
                                                                                                                                                                                                                                                           1998-594563/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
36; Conserv
                                                                                                                                                                                                                                            AAV69887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                          97JP-0151434.
97JP-0217897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-JP01728.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.78;
                                                                                                                                                                                                                                                                                                                                     Kinosaki M,
                                                                                                                                                                                                                                                                                                                    Takahashi K,
                                                                                                                                                                                                                                                                                                Yano K, Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 178; DB 19;
Pred. No. 5.8e-15;
                                                                                                                                                                                                                                                                                                                    Kobayashi F,
, Tomoyasu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                         Morinaga
Tsuda E;
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88888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW69957
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (soBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     components of drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW69957 standard; Protein; 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 SHKYSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NF-kB receptor activator RANK ligand (RANKL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RANKL; RANK ligand; tumour necrosis factor; TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
          This represents a human RANKL, a ligand for the RANK (receptor activator of necrosis factor kappaB (NF kB)) polypeptide. RANK is a activator of the tumour necrosis factor (TNF) family. A soluble RANK member of the tumour necrosis factor (TNF) family. A soluble RANK member of the tumour necrosis factor (TNF) family. A soluble RANK cell may be used for inhibiting activation of NF kB, by contacting a cell may ligand (RANKL). RANKL polypeptides can activate RANK and can be RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their least of the composition of the self or regulating an immune response. The allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an soluble RANK polypeptide composition may also be used for regulating and soluble response that result from triggering of RANK, e.g. in treating toxic response that result from triggering of RANK, e.g. in treating toxic response that result from triggering of RANK, e.g. in treating toxic response and the self-decitions, or acute inflammatory shock or sepsis, graft-versus-host reactions, or acute inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-1997;
                                                                                                                                                                                                                                                                                                                             New isolated ligand for receptor activator of NF-kappa B - used to develop products for augmenting an immune response for inhibiting an inflammatory response and for protection of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                            Claim 27; Pages 59-60; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-377657/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mmune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AHKTSLSSWKHDODWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    AAV41378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
    They can also be used in adjunct therapy for disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galibert LJ, Maraskovsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0059978.
97US-0813509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0064671.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory response; toxic shock; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 178; DB 19;
Pred. No. 5.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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reactions.

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This represents a human RANKL, a ligand for the RANK (receptor activator of necrosis factor kappaB (NF-kB)) polypeptide. RANK is a CC activator of necrosis factor (TNF) family. Host cells transformed the tumour necrosis factor (TNF) family. Host cells transformed CC nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell CC expressing membrane-associated RANK with a soluble RANK which binds to CC used for regulating an immune or inflammatory response. Inhibition of CC NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in CC inflammatory reactions. They can also be used in adjunct therapy for consists can also be used in adjunct therapy for can also be used in adjunct the products
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can also be used for detection and drug screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                          Example 7; Pages 59-60; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              New isolated receptor activator of necrosis factor-kappa B for, e.g. developing products for regulating an immune or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV41372
                                                                                                                                                                                                                                                                                                                                                                              inflammatory response, treating toxic shock or sepsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RANKL; RANK ligand; tumour necrosis factor; TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; infiammatory response; toxic shock; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9828424-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NF-kB receptor activator RANK ligand (RANKL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of manners.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of TNF-alpha. The products can also be used for detection and drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 SHKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Galibert LJ, Maraskovsky E;
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97US-0813509.
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60.08;
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Pred. No. 5.8e-15;
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         The present sequence represents a human osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoplastogenesis in a dose dependent protein. The OPGL protein is synthesised as a type II transmembrane is a potent osteoplast differentiation factor when combined with CSF-1. It is not capable of inducing osteoplast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoplasts. The opglation describes a method for the in vivo down-regulation of DOFL activity in an animal. The method comprises using at least one OPGL an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other alicenses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQ
diseases or conditions characterised by excessive bone resorption
                                                                                                                                                                                                                                                                                                                                     Claim 19; Page 78-79; 110pp; English.
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                                                                                                                                                                                                                                                                                                                                                                        In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to treat, prevent and ameliorate osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ99964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-SEP-1998;
02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MEBI-) M & E BIOTECH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune response; osteoporosis; bone resorption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of a human osteoprotegerin ligand (OPGL).
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60.08;
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Pred. No. 5.8e-15;
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Ax The patent discloses novel receptor activator of nuclear factor (NF)-
CC kappab (RANK) proteins and their corresponding DNAS. RANK is a member of the tumour necrosis factor (TMF) receptor superfamily and associates cult TMF receptor associated factor (TMF) receptor superfamily and associated factor (TMF) response. The important contains the receptors of influence and in screening for inhibitors of signal transduction, e.g. for screening the consequence of inhibitors of signal transduction, e.g. for screening the consequence of the inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, consequence that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, consequence that inhibit interaction of RANK, e.g. in frammatory consequence in a meliorating the negative effects of an inflammatory consequence of the result from triggering of RANK, e.g. in treating toxic consequence in the result from triggering of RANK, e.g. in treating toxic consequence in the result from triggering of RANK, e.g. in treating toxic consequence in the result from triggering of RANK, e.g. in treating toxic consequence in the result of the receptor are used in vivo or in vitro based consequence of the receptor are used in vivo or in vitro based consequence of the receptor are used in vivo or in vitro based consequence of the receptor are used in vivo or in vitro based consequence of the receptor are used in vivo or in vitro based consequence of the receptor are used in vivo or in vitro based consequence of the receptor are used in vivo or in vitro based consequence of the receptor are used in vivo or in vitro based consequence of the receptor are used in vivo or in vitro based consequence of the receptor are used in vivo or in vitro based consequence of the receptor are used in vivo or in vitro based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; receptor activator of nuclear factor kappaB ligand; RANKL; NF; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF; tumour necrosis inflammatory response; graft-versus-host reaction; immune response; inflammatory reaction; bone resorption; toxic shock; sepsis; acute inflammatory reaction; bone resorption; anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE08738 standard; Protein; 317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human receptor activator of NF kappaB ligand (RANKL) protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6271349-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 AHKTSLSSWKHDODWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dougall WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as adjunct therapy for disease characterized by neoplastic cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 15; Column 71-72; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             express RANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 47.7%;
Similarity 60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-520313/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD15311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Galibert L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0077181.
97US-0064671.
96US-0772330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0813509
97US-0996139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0215649.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                             PF XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
   Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transduction of a signal via RANK. RANK compositions are used in the development of both agonistic and antagonistic antibodies, or as an adjunct therapy for disease characterised by neoplastic cells that express RANK. Compounds that interfere with RANK/TRAF6 interactions are useful for modulating the formation of osteoclasts from osteoclast express and for modulating osteoclast function and activities. They are used as inhibitors of diseases associated with excess bone resorption and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are used as inhibitors of anti-inflammatory agents. The proteins are useful for the expression of recombinant proteins, as probes for analysis useful for the expression of recombinant proteins, while the proteins of the presence or distribution of RANK transcripts, while the proteins are useful in preparing kits for the detection of soluble RANK, or are useful in preparing kits for the detection of soluble RANK ligand monitor RANK-related activity. The present sequence is RANK ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RANKL) protein from human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE04426 standard; Protein; 317 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNODGFYYLYANICFRHHETSGDLATEYLOL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; receptor activator of NF-chi B; RANK; tumour necrosis factor; TNF; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; CD40; TNF receptor-associated factor; TRAF; ligand; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human receptor activator of NF-chi B ligand (huRANKL) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6242213-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                               23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-2001
                                                                                                                                                                                                                                                                                                                             14-OCT-1997;
                                                                                                                                                                                                                                                                                             (IMMV ) IMMUNEX CORP.
                                                                                                                                     New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi B receptor activator) of the receptor activator of NF-chi B (RANK)
                                                                                                                                                                                                          WPI; 2001-407216/43.
N-PSDB; AAD08715.
The present invention relates to receptor activator of NF-chi B (RANK) to DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to Chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular
                                                                                                                                                                                                                                                             Anderson DM
                                                                                                       Claim 1; Column 65-66; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        97US-0995659
                                                                                                                                                                                                                                                                                                                                      97US-0064671
                                                                                                                                                                                                                                                                                                                                                                      96US-0059978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Receptor binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
162..317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.7%;
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(1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 178; DB 22;
Pred. No. 5.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 317;
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The present invention relates to a novel receptor, referred to as RANK (receptor activator of NF (nuclear factor) *KappaB), a member of TNF (tumour necrosis factor) receptor superfamily RANK is a Type I can be received in that interacts with TNF receptor associated factors (TRAFS). Triggering of RANK by overexpression or co-expression or co-exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE01993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355555x &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 76-77; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA encoding a receptor activator of NF-kappaB polypeptide for the treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD05904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson DM, Hughes AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; receptor activator of NF-kappaB; RANK; nuclear factor kappaB; NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor associated factor; TRAF; RANK ligand; RANKI; osteopathic; inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial expansile osteolysis; FED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200136637-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human full-length RANKL (receptor activator of NF-kappaB ligand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE01993 standard; Protein; 317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region, RANK associates with TNF receptor-associated factor (TRAF) 2 and TRAF3. The DNA molecules are useful for producing ligands of RANK. The ligands are useful for regulating immune response and in screening for inhibitors of RANK. The present sequence is human RANKL (huRANKL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-329222/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
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Pred. No. 5.8e-15;
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The invention relates to treating an individual at risk for or suffering CC from infection with a pathogenic or opportunistic organism. The method CC involves administering a combination of two to five agents. The method CC agent; (c) dendritic cell mobilisation factor; (b) dendritic cell medicisation agent; (d) Tell administering for treating an individual at risk for or suffering from infection with a CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g. cc useful for treating an individual strikk for or suffering from infection with a CC (e.g. which causes Chaga's disease). The methods are useful for CC centancing a lymphocyte-mediated immune response. In particular, the CC method is useful for treating inflammations, chickenpox, oral or genital CC dendritic cells are useful as a vaccine adjuvant. The presenting cepresents a human RANKL polypeptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB08134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ď
                                                                                                                                                                                                                                                                                                                           Disclosure; Page 42-43; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                   Treating an individual suffering from infection, e.g. inflammation, chickenpox or AIDS, by administering a combination of dendritic cell antigen-specific T cells - returned agent, T cell enhancing factor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-500114/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-NOV-2000; 2000US-245721P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lynch DH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-OCT-2001; 2001WO-US44834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200236141-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial; fungicide; protozoacide; virucide; anti_inflammatory; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human RANKL polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB08134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB08134 standard; protein; 317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 SHKYSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteolysis (FEO) and early onset Paget's disease of bone (EP). The present amino acid sequence is full-length human RANKL (huRANKL) protein. The RANKL gene is located in chromosome 13q14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AHKTSLSSWKHDQDWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           De Smedt TN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317 AA;
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60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 178; DB 22;
Pred. No. 5.8e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miller RE;
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Query Match
Best Local Similarity 60.0%; Pred. No. 5.8e-15;
Mismatches 17; Indels 2; Gaps 1;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

AlkTSLSSWKHDDMANUSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLITLODLQL 60

A AHKTSLSSWKHDDMANUSNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238

Db 179 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238

Db 179 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238

Search completed: December 8, 2002, 19:30:31

Search completed: December 8, 2002, 19:30:31
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OM protein - protein search, using sw model

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

pecember 8, 2002, 17:28:38; Search time 16.2774 Seconds

(without alignments)
221.684 Million cell updates/sec

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Scoring table: Sequence: perfect score:

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.TSAGLTLQDLQLWCNLRIIH 87

us-09-880-457-4

Searched:

Post-processing: Minimum Match 0% Minimum DB seq length: 0
Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries

Database :

SwissProt_40:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Total number of hits satisfying chosen parameters:

112892 seqs, 41476328 residues Gapop 10.0 , Gapext 0.5

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34
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TNII_HUMAN STANDARD; PRT; 317 AA.

O14728; O14723; O99203; O96017;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
16-OCT-2001 (Rel. 41, Last annotation update)
16-OCT-2001 (Rel. 41, Last annotation update)
16-OCT-2001 (Rel. 41, Last sequence update)
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D., Calibart E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Bone marrow, and peripheral blood; MEDLINE=98032977; PubMed=9357155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Lymph node;

MEDLINE-98227661; PubMed-9568710;

Lacey D.L. Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,

Lacey D.L. Timms E., Colombero A., Elliott G., Scully S., Hsu H.,

Burgess T., Elliott R., Colombero A., Elliott G., Eli A., Qian Y.-X.,

Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Delaney J.,

Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                            differentiation and activation."; Cell 93:165-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                "Osteoprotegerin ligand is a cytokine that regulates osteoclast
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
                                                                                                                                                   TISSUB-Thymocytes;

MEDLINE-97460112; PubMed-9312132;

Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Wong B.R., Rho J., Arron J., Bartlett F.S. III, Frankel W.N., Lee S.Y., Kalachikov S., Cayani E., Bartlett F.S. III,
                                                                                                                                                                                                                                                                               Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                         Ikeda T., Kuroyama H., Hirokawa K.;
"Determination of human RANKL isoforms.";
                                                                Choi Y.; "TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal Kinase in T cells."; J. Biol. Chem. 272:25190-25194(1997).
                                                                                                                                                                                                                                           SEQUENCE OF 73-317 FROM N.A.
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Q98631 rice dwarf
P54675 dictyosteli
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p57795 methanosarc
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SEQUENCE FROM N.A. (ISOFORM 2).

TISSUE=Tongue;

"Cancer cells responsible for humoral hypercalcemia express mRNA encoding a secreted form of ODF/TRANCE that induces osteoclast

MEDLINE=20175237; PubMed=10708588; Nagai M., Kyakumoto S., Sato N.;

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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF019047; AAB86811.1; --
EMBL; AF053712; AAC39731.1; --
EMBL; AB064259; BAB79694.1; --
EMBL; AB064277; BAB79695.1; --
EMBL; AB064270; BAB79695.1; --
EMBL; AF013171; AAC51762.1; --
EMBL; AB037599; BAA90488.1; --
                                                   SEQUENCE
                                                                CONFLICT
                                                                              VARSPLIC
                                                                                              VARSPLIC
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                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                               Signal-anchor;
                                                                                                                                                                                                                                                                                  Cytokine;
                                                                                                                                                                                                                                                                                      PROSITE; PS50049; TNF_2;
                                                                                                                                                                                                                                                                                                                 ProDom; PD002012; TNF_abc; 1. SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its early mon-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       ProDom;
                                                                                                                                                                                                                                                                                                                                                                                            MIM; 602642;
                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P50591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catalyzed by ADAM17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are produced by alternative splicing.

TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT
PLACENTA, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.

INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.

PTM: The soluble form of isoform 1 derives from the membrane for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypercalcenia of malignancy.

SUBUNIT: Homotrimer (By similarity).

SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);

Secreted (isoform 2). A soluble form of isoform 1 arises by

Proteolytic processing (By similarity).

ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2/SODF and 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by proteolytic processing (By similarity). The cleavage may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNFRSFILA, TARANK, OSteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chem. Biophys. Res. Commun. 269:532-536(2000).
FUNCTION: Cytokine that binds to TNFRSE11B/OPG and to
                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:11926; TNFSF11.
                                                                                                                                                                                                                                                                                                           PS00251;
                                                                                                                                                                                                                                                                                                                                                                IPR003636; TNF_abc
IPR000478; TNF_fam
                                                                                                                                                                                                                                                      Differentiation; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                      140
                                                                                                                                                69
                                                                                                                                                                                                           Alternative splicing.

1 317 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY

1 STREET TOWNS AND FORM.
                                                                                                                                                                                                                                                                                                                                                    TNF;
                                                                                                                                                                                                                                                                                              TNF_1; FALSE_NEG.
    39.7%; Score 180.5;
                                          35478 MW;
                                                                                                                                                                                                                                                                                                                                                           "NF_family.
                                           MISSING (IN ISOFORM 3).
MISSING (IN ISOFORM 2).
A -> G (IN REF. 4).
                                                                               N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                                                    MEMBER 11, SOLUBLE FORM (BY SIMILARITY).
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                          CLEAVAGE
                                                                                                                                                                                               MEMBER 11, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                             766176446348097F CRC64;
                                                                                                                  (BY SIMILARITY)
    DB 1;
Length 317;
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QΨ
EMBL; AF425669; AAL23963.1;
                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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                                                                                                  Proteolytic processing (By similarity).
                                                                                                                                                                                    -!- PTM: The soluble form derives from the membrane form
                                                                                                                                                 -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
                                                                                                                                                                                                                                                      Marks S.C. Jr.;
"Evidence that the rat osteopetrotic mutation toothless (tl) is not in the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene.";
                                                                                                                                                                                                                                                                                            Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Mason-Savas A., Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 59.7 Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                PubMed=11804028;
                                                                                                                                                                                                                                                                                                                                           STRAIN-Fischer
                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 266-318 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning, sequence and functional characterization of the rathomologue of receptor activator of NF-kB ligand.";
                                                                                                                                                                                                                                                                                                                                                                                                        Zheng M.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20540945; PubMed=11092398;
                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Tibial
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
                                                                                                                               similarity).
TISSUE SPECIFICITY: Highly expressed in thymus and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TN11_RAT
                                                                                                                                                             an important role in enhanced bone-resorption in humoral hypercalcemia of malignancy.
SUBUNIT: Homotrimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                Bone Miner. Res. 15:2178-2186(2000).
             AF187319;
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                                                                                                                                                                                                                                                                                                                                                                                                Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa;
     AAG17031.1; -.
                                                                                                                                                                                                                                                                                                                                          344;
                                                                                                                                                                                                                                                                                                                                                                                                                                  bone;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00251; TNF_1; FALSE_NEG. PROSITE; PS50049; TNF_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                     TNII_MOUSE STANDARD; PRT; 316 AA.

TNII_MOUSE STANDARD; PRT; 316 AA.

O35235; O35236; Q9R1YO; Q9JJK8; Q9JJK9;

16-OCT_2001 (Rel. 40, Created)

16-OCT_2001 (Rel. 40, Last sequence update)

16-OCT_2001 (Rel. 41, Last annotation update)

15-UUN-2002 (Rel. 41, Last annotation update)

Tumor necrosis factor ligand superfamily member 11 (Receptor activator rumor necrosis factor ligand superfamily member 10 (Receptor activator function activator ligand) (RANKI) (TRANCE) (Osteoprotegerin ligand) (OpGL) (Osteoclast of nuclear factor kappa B ligand) (RANKI) (TRANCE) (Osteoprotegerin ligand) (OpGL) (Osteoclast induced cytokine) (TRANCE) (Osteoprotegerin ligand)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 PADYLQL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 IPSISHEAHKTSLSSWKHDQDWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGL
                                                                                                                                                                                                                                                                                                                         differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
                                                                                                                                                                                                                                                                                                  TNFSF11 OR RANKL OR TRANCE OR OPGL.
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 TLODLOL 79
                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                    Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
                                                                                                                                                                                               TISSUE-Hybridoma;
MEDLINE-97460112; PubMed-9312132;
                                                                                                                                                                                                                                                NCBI_TaxID=10090
                                                                                                                                          "TRANCE is a novel ligand of the tumor necrosis factor receptor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00207; TNF;
                                     Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tomotsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                         SEQUENCE FROM N.A. (ISOFORM 1)
 "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
                                                                TISSUE=Thymic lymphoma;
MEDLINE=98032977; PubMed=9367155;
                                                                                                                    Biol. Chem. 272:25190-25194(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Differentiation; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
140
199
264
317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNF_abc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318
                                                                                                                                    c-Jun N-terminal kinase in T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47
68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35370 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11, SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEMBER 11, MEMBRANE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLEAVAGE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 177.5; DB pred. No. 3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I -> M (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4B87AAD706AD098F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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TISUE=Bone marrow;

MEDLINE=98227661; PubMed=9558710;

MEDLINE=98227661; PubMed=9558710;

Lacey D.L., Tilmns E., Tan H.-L., Kelley M.J., Dunstan C.R.,

Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,

Burgess T., Elliott R., Colombero A., Capparelli C., Eli A., Qian Y.-X.,

Sullivan J., Hawkins N., Davy E., Capparelli C., Guo J., Delaney J.,

Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    differentiation and activation cell 93:165-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M., Yasuda H., Shima N., Nakagawa N., Goto M., Murakami A., Tsuda E., Wochizuki S. I. Tomoyasu A., Yano K., Goto M., Suda T.; Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.; Noteoprata differentiation factor is a ligand for "Osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical to TRANCE/RANKL";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Bone marrow stroma;
MEDLINE-98188248; PubMed-9520411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Osteoprotegerin ligand is a cytokine that regulates osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ueda M., Higashio K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1; 2
MEDLINE=21150053; PubMed=11250921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   differentiation factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ikeda I., Kasai M., Utsuyama M., Hirokawa K.;
"Determination of three isoforms of the receptor activator of nuclear
factor kappaB ligand and their differential expression in bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cloning and characterization of the gene encoding mouse osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H., Schloendorff J., Tempst P., Choi Y., Blobel C.P., Brodende of J., Tempst P., Choi Y., Blobel C.P., Providence for a role of a tumor necrosis factor-alpha properting enzyme-like protease in shedding of TRANCE, (TNF-alpha) converting enzyme-like protease in shedding of TRANCE, The family member involved in osteoclastogenesis and dendritic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endocrinology 142:1419-1426(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            survival."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=11581298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316
                                                                                                                                                                                                                         J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
"Crystal structure of the Trance/RankL cytokine reveals determinants
of receptor-ligand specificity.";
J. Clin. Invest. 108:971-979(2001).
                                                                                                                                                                                                                                                                                                  Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.; "Crystal structure of the extracellular domain of mouse RANK ligand
                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
                                                                                                                                                                                                                                                                 2.2-A resolution: ;
2.2-A resolution: ;
3.2-A 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 274:13613-13618(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natl. Acad. Sci. U.S.A. 95:3597-3602(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230:121-127(1999).
   Biol. Chem. 277:6631-6636(2002).

Biol. Chem. 277:6631-6636(2002).

FUNCTION: Cytokine that binds to INFRSF11B/OPG and activation factor. The standard of the standard of the standard of Infrared Tools to Stimulate naive T-cell angments the ability of dendritic cells to stimulate naive T-cell angments the ability of important regulator of interactions augments the ability of an important regulator of interactions and dendritic cells and may play a Tole in the proliferation of the T cell-dependent immune response. May also play regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral an important role in enhanced bone-resorption in humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AND 3).
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1;

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Best Local fimilarity
                                   Query Match
                                                                SEQUENCE
                                                                               CONFLICT
                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                    PDB; 1JTZ; 12-SEP-01
PDB; 1IOA; 13-MAR-02
MGD; MGI:1100089; Tnfsf11
InterPro; IPR003636; TNF-abc.
InterPro; IPR003636; TNF-family.
Pfam; PF00229; TNF; 1
SMART; SM00207; TNF; 1
                                                                                                                           VARSPLIC
                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                 SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF; 1; FALSE_NEG.
PROSITE; PS00251; TNF; 1; FALSE_NEG.
PROSITE; PS50049; TNF; 2; 1.
Cytckine; Differentiation; Receptor; Glycoprotein; Transmembrane;
Cytckine; Differentiation; Alternative splitcing.
Signal-anchor; 3D-Structure; Alternative splitcing.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MFMARANE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF013170; AAC71061.1;
EMBL; AF019048; AAB86812.1;
EMBL; AF053713; AAC40113.1;
EMBL; AB008426; BAA25425.1;
EMBL; AB022039; BAA36970.1;
EMBL; AB022039; BAA36970.1;
JOINED EMBL; AB022031; BAA36970.1; JOINED EMBL; AB022031; BAA36970.1; JOINED EMBL; AB022031; BAA36970.1; JOINED EMBL; AB022031; BAA36970.1; JOINED EMBL; AB022031; BAA36970.1; JOINED EMBL; AB032771; BAA97257.1;
                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I SUCCLULAR LOCATION: Type II membrane protein and secreted (isoforms 1 and 2); Cytoplasmic (isoform 3).

I ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; are produced by alternative splicing.

ITISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS. BUT TRABECULAR BONE AND LUNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PTM: N-91/cosylated.
-!- PTM: The soluble form of isoform 1 derives from the membrane form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by proteolytic processing. The cleavage may be catalyzed by ADAMI?, A further soluble form was observed.
DISEASE DEFICIENCY IN TWESTII RESULTS IN FAILURE TO FORM LOBULO-
ALVEOLAR MAMMARY STRUCTURES DURING PRECNANCY RESULTING IN DEATH
OF NEWBORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEODETROSIS, WITH PROFOUND GROWTH RETARDATION AT SEVERAL SKELTAL SITES, INCLUDING HYPEROFICE, INCLUDING HYPEROFICE, AND VERTEBRAE AND HAVE MARKED CHONDROCYTES, INCLUDING HYPEROFIC CHONDROCYTES.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: Homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB032772; BAA97258.1;
AB036798; BAA97259.1;
LJTZ: 12-CED-01
                                                         316 AA;
                                                                                           99
                                                    34944 MW;
Pred. No. 4.4e-13;
                Score 176;
                                                           G -> D (IN REF. 2)
MISSING (IN REF. 5)
                                                                                      SSEEMGSGPGVPHEGPLHPAPSAPAPAPPPA -> TP (IN
                                                                                                                 MISSING (IN ISOFORM 3)
                                                                                                                              N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                             MEMBER 11, SOLUBLE FORM.

CYTOPLASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                       MEMBER 11, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                   08DF63A2BE00967A CRC64;
      Length 316;
                                                                                                                                        (POTENTIAL).
                                                                                                                         (POTENTIAL).
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Nelson B.;
Unpublished observations (SEP-2000).
-1- FUNCTION: MAY BE INVOLVED IN THE METABOLISM OF INSECT HORMONES AND
IN THE BREAKDOWN OF SYNTHETIC INSECTICIDES (BY SIMILARITY).
                                         CONCEPTUAL TRANSLATION
                                                                                                                                                                                                                                                                                                                                                                                                      CSD2_DROME
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly),
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Hexapoda;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     To-OCT-2001 (Rel. 40, Last annotation update)
Probable cytochrome P450 28d2 (EC 1.14. . . . ) (CYPXXVIIID2).
                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                CSD2_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                        173 ŚIPSGSHKVTLSSWYHDRGWAKIŚNWTLŚNGKĹRVNODGFYYLYANICFRHHETŚGSVPT 232
                                                                                                                                                                                                                                                                                                                                                                                                                              233 DYLQL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                17 SISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SC65_YARLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institutions as long as its content is in no way used by non-profit institutions as long as its content is in no way used that the content is a second to the content in the content is an example of the content is a second to the content is a se
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-i- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH + oxidized flavoprotein + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0031688; Cyp28d2.
InterPro: IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE003609; AAF52225.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome; Endoplasmic reticulum; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEC65 OR SRP19.
Yarrowia lipolytica (Candida lipolytica)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SC65_YARLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 KERRSEIMPALSPNRVKAVYPVSQSVCKKFVEYIRRQQQMATSEGLDAMDLSLCYTTEVV 192
                                                                                                                                                                                                                                                                                                                                                                                                                        Sanchez M., Beckerich J.M., Gaillardin C., Dominguez A., "Isolation and cloning of the Yarrowia lipolytica SEC65 gene, a component of the yeast signal recognition particle displaying homology with the human SRP19 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 20460 / W29;
MEDLINE-98085978; PubMed-9426009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 -----RVKGIYYRNADICSR------HRVTSAGLTLQDLQLWCNLRII 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 VGVFTTRVPQLLVMCPEYIHKIYATDFRSF-HNNEWRNFVNKKTDMILGNNPFVLTGDEW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAUTION: Ref.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene model prediction.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                         Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pocar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAILTLSLQLTLLLIPSISHEAHKTSLSSWKHDQDWANVSN----WTFSNGKL------ 49
                                                                                                                                                                               e 203:75-84(1997).

E CONCITION: SIGNAL-RECOGNITION-PARTICLE ASSEMBLY HAS A CRUCIAL ROLE FUNCTION: SIGNAL-RECOGNITION-PARTICLE ASSEMBLY HAS A CRUCIAL ROLE FUNCTION: SIGNAL RECOGNITION THE TRANSLOCATION OF A MEMBRANE. IT MUST BE INVOLVED INTIMATELY IN THE TRANSLOCATION OF A MEMBRANE. IT MUST BE INVOLVED INTIMATELY IN THE TRANSLOCATION OF A 7S RNA SUBBURIT: FUNGAL SIGNAL RECOGNITION PARTICLE CONSISTS OF A 7S RNA SUBBURIT: SUBGRAL RECOGNITION PROTEIN SUBGRATIS: SRP72, SRP68, MALECULE (SCR.) AND AT LEAST SEVEN PROTEIN SUBGRATION SRP72, SRP68, MALECULE (SCR.) AND AT LEAST SEVEN PROTEIN SUBGRATION OF A THE STREET OF A TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recognition particle SEC65 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58222 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.3%; Score 78.5; DB 1; 20.0%; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9AD85F249390A655 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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NU5M_ALLMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z22570; CAA80293.1; ... InterPro; IPR002778; SRP19. pfam; PF01922; SRP19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal recognition particle; RNA-binding; Ribonucleoprotein. SEQUENCE 310 AA; 35487 MW; D65EC9F0C80114C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01922; SRP19; 1.
ProDom; PD006609; SRP19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p50365;

01-0CT-1996 (Rel. 34, Last sequence update)

01-0CT-1996 (Rel. 37, Last annotation updat

15-DEC-1998 (Rel. 37, Last annotation (EC
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NU5M_ALLMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 MLTLPSI-YEAHKT-----HPKDWAN-----PGRVRVQ 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC 46923 / BURMA 3-35 (350C);
paquin B., Roewer I., Wang Z., Lang B.F.;
"A robust fungal phylogeny using the mitochondrially encoded nad5
protein sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            עבע באס (גרבו. אוי, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
ND5 OR NAD'5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Chytridiomycota; Blastocladiales; Blastocladiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Allomyces macrogynus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=28583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 LLLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK 52
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 46923 / BURMA 3-35 (350C);
MEDLINE=96226032; PubMed=8636971;
                                                                                                                                                                                                                                                                                                                                  gequence from an ancestral fungus.";
J. Mol. Biol. 255:688-701(1996).
-i- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                   "The mitochondrial DNA of Allomyces macrogynus: the complete genomic
                                                                                                           Interpro; IPR003916; NADHub_oxred5.
Interpro; IPR001750; Oxidored_q1.
Interpro; IPR001516; Oxidored_q1_N.
                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                         EMBL; U17010; AAB05846.1; EMBL; U41288; AAC49228.1;
                                oxidoreductase; NAD; Ubiquinone; Mitochondrion SEQUENCE 641 AA; 70674 MW; 9C64C376B72E7E6
                                                              PRINTS; PR01434; NADHDHGNASE5
                                                                                 pfam; pr00361; oxidored_q1; 1.
pfam; pr00662; oxidored_q1_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bot. 73:S180-S185(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 14.5%;
Similarity 41.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
          14.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 66; DB 1
pred. No. 2.4;
            Score 65.5; DB 1; Length 641;
                                           9C64C376B72E7E61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   641 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ω
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Best Local Similarity

Conservative

12; Pred.

Mismatches No. 6.5;

28;

27.9%;

В

CHLTR

108_CHLTR

Вb

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GUB_CLOTM STANDARD; PKI; JJ* G...
P29716; p37074;
01-APR-1993 (Rel. 25, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                  148 SQLSAYYQTPVLAKALGGKKRVSSAAL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGRO0486; DUF34; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE001284; AAC67699.1; -. PHCI-2DPAGE; O84110; -.
                                                                                                                                                                                                                                                  55 -----YYRNADIC----SRHRVTSAGL 72
                                                                                                                                                                                                                                                                    91 NIQLIAYHLPL---DAHTTIGNNWKVARDLGWEQLESFGSSQPSLGVKGVFPEMEVHDFI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99000809; PubMed-9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aray
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                   7 SLOLILLLIPSISHEAHKTSLSSWK--HDQDWANVSNWTFSNGKLRVKGI------ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia trachomatis.
Bacteria; Chlamydiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   582 GIFARDID 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            522 SLLGISLALIVLKDPKKMHSIEKPEGLLNTVNITRWLSSKSYWEDNVYNTVLISGSLHFG 581
                                                                                                                                                                                                                                                                                                                                                                                              lete proteome.
ENCE 251 AA; 27474 MW; A4C2F6BE7517298E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 GIYYRNAD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pro; IPR002678; DUF34.
PF01784; DUF34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AILTLSLQLILLLIPSISHEAHK-----TSLSSWKHDQDW--ANVSNMTFSNGKLRVK 52
                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282:754-759(1998)
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                        14.3%; Score 65; DB 1; Length 251; 26.4%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 AA.
                                                                                                                                                                                                                                                                                                                                              27;
                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aravind L.,
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9;
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                                                                                                                                                                                                                                                                                                                                     4;
                            ACT_SITE
ACT_SITE
                                     DOMAIN
                                                                                                                                                                                                                                                                                 PIR; S23498; S23498
PIR; JS0611; JS0611
PIR; S18726; S18726
HSSP; P23904; LAJK
                          DOMAIN
                                                                                                         SIGNAL
                                                                                                                       PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1. PROSITE; PS00448; CLOS_CELLULOSOME_RPT; 2.
                                                                                                                                                                           Pfam; PF00404; Dockerin 1; 2. pfam; PF00722; Glyco_hydro_11; 1. PRINTS; PR0737; GLHYDRLASELS.
                                                                                           CHAIN
                                                                                                                                                                                                         InterPro; IPR002105; Dockerin_1.
InterPro; IPR002048; EF-hand.
InterPro; IPR000757; Glyco_hydro_16.
Pfam: PF00404; Dockerin_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.lsb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                              EMBL; X63355; CAA44959.1; -...EMBL; X58392; CAA41281.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zveilov V. V. Velikodvorskaja G.A.;

"Cloning the Clostridium thermocellum thermostable laminarinase gene in Escherichia coli; the properties of the enzyme thus produced.";

in Escherichia (12:811-816(1990)).

-i- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.

-i- SUBUNIT: MAY FORM PART OF A MULTIENZYME COMPLEX (CELLULOSOME).

WELL AS IN OTHER C.THERMOCELLUM CELLULOSOME INTHIS ENZYME AS MAY FUNCTION AS THE BINDING LIGAND FOR THE SL COMPONENT.

MAY FUNCTION AS THE BINDING LIGAND FOR THE SL COMPONENT.

-i- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zverlov V.V., Laptev D.A., Tishkov V.I., Velikodvorskaja G.A.; "Nucleotide sequence of the Clostridium thermocellum laminarinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zverlov V.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 181:507-512(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 27405 / DSM 1237;
MEDLINE-92155194; PubMed=1740123;
Schimming S., Schwarz W.H., Staudenbauer W.L.;
"Structure of the Clostridium thermocellum gene licB and the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92095946; PubMed=1755832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lichenases joined to the reiterated domain of clostridial cellulases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eur. J. Biochem. 204:13-19(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-1,3-1,4-glucanase. A catalytic region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase) (Laminarinase).
LICB OR LAM1.
                                                                                                                  Glycosidase;
                       28
136
140
252
273
                   334
136
140
269
331
                                                                                                           Signal; Repeat.
BETA-GLUCANASE.

NUCLEOPHILE (BY SIMILARITY).

PROTON DONOR (BY SIMILARITY).

PRO/THR-RICH (LINKER).

2 X 24 AA APPROXIMATE REPEATS.
                                                                                            POTENTIAL.
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RESULT 8
GUB_CLOTM

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Matches

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Query Match

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                                                          Matches
                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
0rotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)
(OMPDCase) (OMPdecase) (Uridine 5'-monophosphate synthase) (UMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                      Appl. Microbiol. Biotechnol. 40:361-364(1993).
-i- CATALYTIC ACTIVITY: Orotidine 5'-phosphate = UMP + CO(2).
-i- PATHWAY: Pyrimidine biosynthesis; sixth (last) step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene replacement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Merckelbach A., Goedecke S., Janowicz Z.A., Hollenberg C.P.; "Cloning and sequencing of the ura3 locus of the methylotrophic yeast Hansenula polymorpha and its use for the generation of a deletion by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pichia angusta (Yeast) (Hansenula polymorpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYRF_PICAN
Q06375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PICAN
                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94128354; PubMed=7764392;
                                                                                                                                                                                                                         EMBL; X69461; CAA49221.1; -. PIR; S31323; S31323.
                                                                                                                   SEQUENCE
                                                                                                                                   Pyrimidine biosynthesis; Lyase; Decarboxylase.
ACT_SITE 92 92 BY SIMILARITY.
                                                                                                                                                                               Pfam;
                                                                                                                                                                 PROSITE;
                                                                                                                                                                                             InterPro; IPR001754; OMPdecase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 KPSQVTFSNGKM 76
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 90
                            3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAILTLSLQLILLLIPSISHEAHKTSL-------SSWKHDQDWAN-----
                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE OMP DECARBOXYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -VSNMTFSNGKL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISLIMASLILIVISVIVAPFYKAEAATVVNTPFVAVFSNFDSSQWE-KADWANGSVFNCVW 64
DRKFADIGNTV----KLQYKGGIYRTSKWADITNAHGVTGAGI 128
                          DQDWANVSNMTFSNGKLRVKGIYYRN---ADICSRHRVTSAGL 72
                                                                                                                                                                                                           P03962; 1DQW
                                                                                                                                                                             PF00215; OMPdecase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                        Similarity
                                                                                                                                                               PS00156; OMPDECASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 AA;
                                                                                                                    263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273
308
304
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                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37897 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.1%;
27.8%;
                                                                                                                    29275 MW;
                                                                       14.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 64; DB 1; Length 334; Pred. No. 4.6;
                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.
2.
QSVADVNRDGRIDSTDLTMLKRYLIRAIPSL ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PODGCGRHDRVVDSGSK (IN REF. 2 AND
                                                                       Score 63.5;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0837564E9726F281 CRC64;
                                                                                                                    0934EF673B03A820 CRC64;
                                                            Mismatches
                                                                                                                                                                                                                                                                                                               There are no restrictions ng as its content is in
                                                                        .9;
                                                                                      DB 1;
                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                    Usage
                                                                                      Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT 10
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                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Rd / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed=7542800;

Fileischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

Kerlavage A.R., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Weidman J.F., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical HI1656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P45300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YRAN_HAEIN
                                                                                 O9XS77;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Interleukin-1 beta precursor (IL-1 beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U32838; AAC23300.1; -. TIGR; HI1656; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae
              Trichosurus vulpecula (Brush-tailed possum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Complete SEQUENCE 119 AA; 13812 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGREAMS; TIGRO0252; TIGRO0252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003509; UPF0102.
Pfam; PF02021; UPF0102; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: BELONGS TO THE UPF0102 FAMILY. STRONG,
NCBI_TaxID=9337;
                                                                                                                                                                        IL1B_TRIVU
                                                                                                                                                                                                                                                            102 IAFGKTPQDIQ-W 113
                                                                                                                                                                                                                                                                                                                                                            10 LILLLIPSISHEAHKTSLSS--WKHDQDWANVSNMTFSNGKLRVKGIYYRNADICSRHRV 67
                                                                                                                                                                                                                                                                                                                                 49
                                                                                                                                                                                                                                                                                              68 TSAGLTLQDLQLW 80
                                                                                                                                                                                                                                                                                                                               IVFVEVRQRSHSAYGSAIESVDWRKQQKWLDAANLWLAKQNMSLE-----DANCRFDL 101
                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 32, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                    13.8%;
21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 63; DB 1; Length 119; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteome.
B7359D8181F31AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                          269 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TO E.COLI YRAN.
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InterPro; IPR003502; IL1_propep.
InterPro; IPR000975; Interleukin_1.
Pfam; PF00340; IL1; 1.
Pfam; PF02394; IL1_propep; 1.
PRINTS; PR00262; IL1HBGF.
ProDom; PD002536; Interleukin_1; 1.
                             Streptomyces clavuligerus.
Bacteria; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                     IPNS_STRCL STANDARD; P10621; P10621; O1-JUL-1989 (Rel. 11, Created) O1-JUL-1989 (Rel. 11, Last sequing the sequing term of the
        Actinomycetales; Streptomycineae;
                                                                                                                                   synthase).
                                                                                                         PCBC
                                                                                                                                                                                                                                                                                                                               STRCL
                                                                                                                                                           Isopenicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytokine; Macrophage; Mitogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00253; INTERLEUKIN_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00125; IL1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF071539; AAD21871.1; -. HSSP; P01584; 1HIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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SEQUENCE FROM N.A.
MEDLINE-99221044; PubMed-10206203;
Wedlock D.N., Goh L.P., Parlane N.A., Buddle
                                                                                                                                                                                                                                                                                                                                                                                                                                                  123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning and physiological effects of brushtail possum interleukin-lbeta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 LLLIPSISHEAHKTSLSS-WKHDQDWANVSNMTFSNGKLRVKGIYYRNADI----CSRHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Immunol. Immunopathol. 67:359-372(1999).

FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY. IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE IL-1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION. MISCELLANEOUS: THE LACK OF A SPECIFIC TYPHOSOPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                         VSSQDCTIQDINQKCLALSKASELRALH 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTSAGLTLQDLQLWC-----NLRIIH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VMVIVAIEKMKHLNGLSSQFFQDNDLMNIFTNIFQE-----EPITFKNCDIYESDSSFRL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETORY PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                        (Rel. 11, Last sequence update)
(Rel. 38, Last annotation update)
in N synthetase (EC 1.-.-.-) (IPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269
31141 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.5%; Score 61.5; D 27.3%; Pred. No. 6.9;
                                                                                                                                                     (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n; Inflammatory response; Pyrogen BY SIMILARITY.
INTERLEUKIN-1 BETA.
                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                               1.-.-.) (IPNS) (Isopenicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTERLEUKIN-1 BETA.
307A1FE3B627D6E7 CRC64;
     Streptomycetaceae;
                                                                                                                                                                                                                                                                                                  329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
     Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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CYA7_BOVIN
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                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             Best
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M19421; AAA26770.1; -.
EMBL; A01132; CAA00131.1; -.
PIR; A29894; A29894
HSSP; P05326; 1BLZ.
InterPro; IPR005123; 2OG-FEII_Oxy.
InterPro; IPR002283; IPM_synth.
InterPro; IPR002287; Isopen_M_synth.
Pfam; PF03171; 2OG-FEII_Oxy; 1.
PSTANCE.
                                                                                                                                        CYA7_BOVIN STANDARD; PRT; 1078 AA 029450; 002856; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update)
SEQUENCE FROM N.A
                                            Mammalia; Eutheria;
Bovidae; Bovinae; Bo
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                Adenylate cyclase, type VII (EC 4.6.1.1) (ATP (Adenylyl cyclase).
                            NCBI_TaxID=9913;
                                                                                       Bos taurus (Bovine).
                                                                                                          ADCY7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin METAL 212 212 IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00185; IPNS_1; PROSITE; PS00186; IPNS_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "CLORING and nucleotide sequence determination of the isopenicillin synthetase gene from Streptomyces clavuligerus."; Gene 62:187-196(1988).

-!- FUNCTION: REMOVES, IN THE PRESENCE OF OXYGEN, 4 HYDROGEN ATOMS FROM DELTA-L-(ALPHA-AMINOADIPYL)-L-CYSTEINYL-D-VALINE (ACV) TO FORM THE AZETIDINONE AND THIAZOLIDINE RINGS OF ISOPENICILLIN.
                                                                                                                                                                                                                                                                                          115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leskiw B.K., Aharonowitz Y., Mevarech M., Wolfe S., Vining L.C., WestLake D.W.S., Jensen S.E.; "Cloning and nucleotide sequence determination of the isopenicil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- COFACTOR: IRON AND ASCORBATE.
-!- PATHWAY: CENTRAL ROLE IN THE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 27064 / DSM 738 / NRRL 3585; MEDLINE=88212175; PubMed=3130293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
STRAIN=ATCC 27064
                                                                                                                                                                                                                                                                                                                                                    55
                                                                                                                                                                                                                                                                                                                                                                         15 IPSISHEAHKTSLSSWKHD------QDWANVSNMTFS--NGKLRVKGIYYRNADICSRH 65
                                                                                                                                                                                                                                                                                                                     66 RVTSAGLTLQDLQLW 80
                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                           LQDVVNEFHGAMTDQEKHDLAIHAYNPDNPHVRNGYYKAVPGRKAVESFCYLNPDFGEDH 114
                                                                                                                                                                                                                                                                                      PMIAAGTPMHEVNLW 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEPHALOSPORIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M19421; AAA26770.1;
                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                          Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268
329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPNSYNTHASE.
                                            Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214
268
                                                       Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36958 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                          13.5%;
24.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 61.5;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71AA1CCE9514761C
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                       Ruminantia;
                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                pyrophosphate-lyase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                     Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PENICILLIN AND
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O
                                                     Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                NUD1_YEAST
                                                                                            RESULT 14
                                                                                                                                                                                                                                                                      Query Match
NUD1_YEAST STANDARD; PRT; 851 AA. P32336; Q08895; Q1-CCT-1993 (Rel. 27, Created) Q1-NOV-1997 (Rel. 35, Last sequence update) Q1-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001054; G_cyclase. Pfam; PF00211; guanylate_cyc; 2. SMART; SM00044; CYCC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1. PROSITE; PS50125; GUANYLATE_CYCLASES_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                             791 WHLKTMTNFYLVLFYTTLIMLSRQIDYYCRL 821
                                                                                                                                                                               739 MSLELKYVLLTVALVAYLVLFNVYPSWQWDCCGHSLGNLTGTNGTL----
                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z49806; CAA89894.1; ALT_INIT.
HSSP; P26769; IAB8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- FUNCTION: THIS A MEMBRANE-BOUND, CA(2+)-INHIBITABLE ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Voelkel H., Beitz E., Klumpp S., Schultz J.E.; "Cloning and expression of a bovine adenylyl cyclase type VII specific to the retinal pigment epithelium."; FEBS Lett. 378:245-249(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96149441; PubMed=8557110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Retina
                                                                                                                                                              64
                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                       4 LTLSLQLILLLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVKGIYYRNADICS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPITHELIUM.

DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.

SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein. TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE RETINAL PIGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate
                                                                                                                                                        RHRVTSAGLTL------QDLQLWCNL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAMP synthesis; Transmembrane;
                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                1078
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                           34
63
95
125
150
176
176
197
197
595
669
718
                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           33
54
83
120
145
170
                                                                                                                                                                                                                                                     13.5%;
20.9%;
                                                                                                                                                                                                                                                                                           120819 MW;
                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                   Score 61.5;
Pred. No. 34;
                                                                                                                                                                                                                                                                                       N-LINKED (GLĆNAC. . .) (POTENTIAL).
N-LINKED (GLĆNAC. . .) (POTENTIAL).
N-LINKED (GLĆNAC. . .) (POTENTIAL).
MW; 50E89BF08E37FCBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Repeat.
                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                      34;
                                                                                                                                                                                                                                                               Length 1078;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL outstation
                                                                                                                                                                                                                                    19;
                                                                                                                                                                                -SSSSCS 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration
                                                                                                                                                                                                                                  Gaps
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GLT1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                         GLT1_YEAST STAN
Q12680; Q12290;
01-NOV-1997 (Rel. :
01-NOV-1997 (Rel. :
30-MAY-2000 (Rel. :
                                                             Filetici P., Martegani M.P., Valenzuela L., Gonzalez A., Ballario P. "Sequence of the GLT1 gene from Saccharomyces cerevisiae reveals the domain structure of yeast glutamate synthase.";
STRAIN=S288c;
                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharon Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                  Glutamate synthase [NADPH] precursor (EC 1.4.1.13) (NADPH-GOGAT). GLT1 OR YDL171C.
                 SEQUENCE FROM N.A.
                                                                                                                                      MEDLINE=97082505; PubMed=8923741;
                                                                                                                                                              STRAIN-CN36
                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                       Yeast 12:1359-1366(1996).
                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X62147; CAA44073.1; -. EMBL; Z75281; CAA99704.1; -. PIR; S19056; S19056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/orsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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Submitted (JUL-1996) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 QLILLLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLR----------
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rPro; IPR001611; LRR.
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                                                                                                                                                                                                                                                                                                                                       35, Created)
35, Last sequence update)
39, Last annotation updat
                                                                                                                                                                                                                                                       Ascomycota; Saccharomycotina; Saccharomycetes;
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23.5%;
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Pred. No.
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CB9F0408633C1315 CRC64;
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EMBL; Z67750; CAA91574.1; -.
EMBL; Z74219; CAA99745.1; -.
SGD; S0002330; GLT1.
InterPro; IPR002489; DUF14.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR002932; Glu_synthase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00070; pyr_redox; 1.
Pfam; PF01493; DUF14; 1.
Pfam; PF01645; Glu_synthase; 1.
ProDom; PD000139; FAD_pyr_redox; 1.
TIGRFAMs; TIGR01317; GOGAT_sm_gam; 1.
Oxidoreductase; Iron_sulfur; 3Fe-4S; Flavoprotein; FAD; FMN; NADP;
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                                                                                                                                                                                                                                       348 TLSLPEAVMMMVPEAYHKDMDSDLKAW-YDWAACLMEPWDGPALLTFTDGRYCGAILDRN 406
                                                                                                                      407 GLRPCRYYITSDDRVICA 424
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nes 20; Conserv
                                                                                                                                                                             53 GI----YYRNAD---ICS 63
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1184 IRON-SULFUR (3FE-4S) (BY SIMILARITY).

1190 IRON-SULFUR (3FE-4S) (BY SIMILARITY).

1195 IRON-SULFUR (3FE-4S) (BY SIMILARITY).

30 L -> D (IN REF. 2).

172 TSRRFYY -> NVPVDSTI (IN REF. 2).

451 IPS -> FLV (IN REF. 2).

1752 L -> V (IN REF. 2).

1752 L -> V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                   13.4%; Score 61; DB 1; Length 2144; 25.6%; Pred. No. 86;
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OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2002 Compus
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ALIGNMENTS

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RESULT 1
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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: E72203
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: E72203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: Pyrococcus horikoshii hypothetical protein PH1107
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A; Residues: 1-296 <ARN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer, submitted to the Protein Sequence Database, January 2000 A;Reference number: 223021 A;Reference number: 745103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T25B15.100 - Arabidopsis thaliana hypothetical protein T25B15.100 - Arabidopsis thaliana (mouse-ear cress) c;Species: Arabidopsis thaliana (mouse-ear cress) c;Pate: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000 c;Pate: 04-Feb-2001 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000 c;Pate: 04-Feb-2001 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000 c;Pate: 04-Feb-2001 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000 #sequence_revision 04-Feb-2000 #sequence_revi
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                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-307 <ALC>
A; Cross-references: EMBL:AL132972
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                                                                                                                              A; Map position: 3
A; Introns: 63/3; 2
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                                                                                       A; Note: T25B15.100
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 DODW---ANVSNMTFSNGKLRVKG---TYYRNADICSRHRVTSAGLTLQDLQLWC 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.7%; Score 67; DB 2; Length 296; ilarity 27.3%; pred. No. 5.4; Conservative 11; Mismatches 19; Indels
                                                                                                                                                 225/2; 267/3
                             14.7%; Score 67;
                                                DΒ
                                                2;
                                           Length 307;
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R;Sanchez, M.; Beckerich, J.M.; Gaillardin, C.; Dominguez, A. Gene 203, 75-84, 1997
A;Title: Isolation and cloning of the Yarrowia lipolytica SEC65 gene, a component of the A;Reference number: JC6516; MUID:98085978; PMID:9426009
                                      A;Cross-references: EMBL:Z22570; NID:g473182; PID:g473183
                                                                             A; Molecule type: DNA
A; Residues: 1-310 <SAN>
                                                                                                                                                                                                                                                                               signal recognition particle protein Sec65 - yeast (Yarrowia lipolytica)
N.Alternate names: SRP19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
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                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                             ;Species: Yarrowia lipolytica, Candida lipolytica
;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 23-Jul-1999
;Accession: JC6516; S44157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Reference and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: B96615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-286 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable carbonic anhydrase T18124.9 [imported] - Arabidopsis thaliana C;Speckes: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: B96615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                  278 YISDREIW 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 CRNCEKESIKDSVMNLITYSWIRDRVKRGEVKIHGCYYNLSD-CSLEKWRLSSDKTNYGF 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 AVTTLQVENIIVMGHSNCGGIAALMSHQNHQGQHSRWVMNGKAAKLRTQLASSHLSFDEQ 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 TLQDLQLW 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 WAN-----VSNM-TFS-----NGKLRVKGIYYRNADICSRHR-----VTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AILTLSLQLILLLIPS-----ISHEAHKTSLSSW------KHDQD 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 AWTDDKCVLMSFDLTSEDVGVW 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 HDEYKVLSFIWRHNKEWKVRSEHHVLVLGARTSWKKTOCHIHHLPVSQG-ITINGVLYYG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 ADICSRHRVTSAGLTLQDLQLW 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 HEAHKTSLSSWKHDQDW--------ANVSNWTFSNGKLRVKGIYYRN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                 :4.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.5%; Score 66; DB:
21.1%; Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.3%; ***
        Score 66; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 5.7;
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Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
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probable ACR - Chlamydia trachomatis (serotype D, strain UW3/Cx)
                                                                                                                                   В
                                                                        RESULT 7
                                                                                                                                                                                                                                                                                                                   A; Experimental source: cultivar Columbia; BAC clone T9A21
                                                                                                                                                                                                                                                                                   A; Note: T9A21.160
                                                                                                                                                                                                                                                                                                      A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: AL021713
                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-210 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                              C:Accession: T04933
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, February 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T9A21.160 - Arabidopsis thaliana c;Species: Arabidopsis thaliana (mouse-ear cress) c;Species: Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999 C;Accession: T04933
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                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                             Query Match
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A:Introns: 144/3; 241/3; 314/1
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U41288; NID:g1236403; PIDN:AAC49228.1; PID:g1236411
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-641 <PAQ>
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U. MOl. Biol. 255, 688-701, 1996
A;Title: The mitochondrial DNA of Allomyces macrogynus: the complete genomic sequence
A;Reference number: S63635; MUID:96226032; PMID:8636971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Allomyces macrogynus mitochon C:Species: mitochondrion Allomyces macrogynus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                               101 IPTHNLPVVGSTIDSISPSADKISIIGWGHSEDETFQSQDW-NVININYT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 41.5%; Pred. No. 7.5; Matches 17; Conservative 7; Mismatches
                                                                                                                                       3 ILTLSIQLILLLIPSISHEAHKTSLSSWKH-----DQDWANVSNWTFS 45
                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     582 GIFARDID 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522 SLÉGISÉALÍVÉKDÞKKMHSIEKÞEGLLNTVNITRWLSSKSYWFDNVYNTVLISGSEHFG 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 GIYYRNAD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AILTLSLQLILLLIPSISHEAHK-----TSLSSWKHDQDW--ANVSNMTFSNGKLRVK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 LLLIPSISHEAHKTSLSSWKHDQDWANVSNWTFSNGKLRVK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                       14.3%; Score 65; DB 36.0%; Pred: No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.4%; Score 65.5;
27.9%; Pred. No. 20;
                                                                                                                                                                             8; Mismatches 16; Indels
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                                                                                                                                                                                                                     DB 2; Length 210;
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                                                                                                                                                                               8,
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                                                                                                                                                                       Gaps
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C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C;Accession: C71557
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Ritle: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tracellular pathogen number: A71570; MUID:99000809; PMID:9784136
A;Accession: C71557
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C; Superf
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A;Cross-references: GB:AE001284; GB:AE001273; NID:g3328494; PIDN:AAC67699.1; PID:g33285(A;Experimental source: serotype D, strain UW-3/Cx
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; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl.
A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable glucanotransferase (endo alpha-1,4 polygalactosaminidase related protein) [impd C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: E96990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
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                                                                                                                                                                                                                                                                                                                                                                                   acetylornithine deacetylase BH2678 [imported] - Bacillus halodurans (strain C-125) (;Species: Bacillus halodurans (c;Species: Bacillus halodurans (c;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 17-May-2002 C;Accession: F83984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE001437; PIDN:AAK78712.1; PID:g15023617; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-276 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: E96990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: CAC0736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                          R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete yenome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete yenome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete yenome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete yenome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete yenome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete yenome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete yenome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete yenome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete yenome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete yenome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete yenome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete yenome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete yenome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete yenome yen
A; Molecule type: DNA
A; Residues: 1-427 <STO>
                                                                                                                                         A; Reference number: A83650; MUID:20512582; PMID:11058132
A; Accession: F83984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 14.3%; Score 65; DB:
Local Similarity 26.4%; Pred. No. 7.6;
Les 23; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 NWK-DESWIDVSNLKWDNYVVNTLGKNLKNKGVDGFFLDNLDVYSKYKKDSMFIGLLNI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 NIQLIAYHLPL---DAHTTIGNNWKVARDLGWEQLESFGSSQPSLGVKGVFPEMEVHDFI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 ----YYRNADIC----SRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 SLQLILLIPSISHEAHKTSLSSWK--HDQDWANVSNMTFSNGKLRVKGI------ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 SWKHDQDWANVSNMTFSN-----GK-LRVKGI---YYRNADICSRHRVTSAGLTLQDL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.2%; Score 64.5; D
30.5%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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A;Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06397.1; GSPDB:G
A;Experimental source: strain C-125
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C;Superfamily: succinyl-diaminopimelate desuccinylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Schimming, S.; Schwarz, W.H.; Staudenbauer, W.L.

Eur. J. Biochem. 204, 13-19, 1992

A;Title: Structure of the Clostridium thermocellum gene licB and the encoded beta-1,3

1 cellulases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Clostridium thermocellum C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: S23498; S22137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     licheninase (EC 3.2.1.73) licB precursor - Clostridium thermocellum N; Alternate names: beta-1,3-1,4-glucanase licB; lichenase licB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: licheninase licB; Clostridium cellulase repeat homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;1-27/Domain: signal sequence #status predicted <SIG>F;28-334/Product: licheninase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: S23498; MUID:92155194; PMID:1740123 A;Accession: S23498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X63355; NID:g40697; PIDN:CAA44959.1; PID:g40698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-334 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;28-334/Product: licheninase #Status predicted Small
F;273-296/Domain: Clostridium cellulase repeat homology
F;308-331/Domain: Clostridium cellulase repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: licB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                           orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - yeast (Pichia angusta) C;Species: Pichia angusta C;Species: Pichia angusta C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000
                                                                                                                                             A;Description: Cloning and A;Reference number: S31323 A;Accession: S31323
A;Cross-references: EMBL:X69461; NID:g2783; PIDN:CAA49221.1; PID:g2784 C;Superfamily: orotidine-5'-phosphate decarboxylase; orotidine-5'-phosphate decarboxy
                                                           A; Molecule type: DNA
A; Residues: 1-263 <MER>
                                                                                                                                                                                                                                      R;Merckelbach, A.; Goedecke, S.; Janowicz, Z.A.; Hollenberg, C.P. submitted to the EMBL Data Library, November 1992
                                                                                                                                                                                                                                                                                               C; Accession: S31323
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
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                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           407 LVQYTKTLLTF -- IYEWCHLR 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 RHRVTSAGLTLQDLQLWCNLR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 SLQLILLIPSISHEAHKTSLSSWKHDQDW---ANVSNMTFSNGKLRVKGIYYRNADICS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 14.28; Score 64.5; Local Similarity 27.28; Pred. No. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 KPSQVTFSNGKM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 -VSNMTFSNGKL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 14.1%; Score 64; DB 1; Length 334; Local Similarity 27.8%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 ISLLMASLLLVLSVIVAPFYKAEAATVVNTPFVAVFSNFDSSQWE-KADWANGSVFNCVW 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAILTLSLQLILLLIPSISHEAHKTSL-------SSWKHDQDWAN------ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                   sequencing of the URA3 locus of the methylotrophic yeast H
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                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-813 <STO>
                                                                                                                                                                                                                                                                                  A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83476
                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83476
                                                                                                                                                                                                A;Cross-references: GB:AE004565; GB:AE004091; NID:g9947294; PIDN:AAG04754.1; GSPDB:GN00
                                                                                                                                                                                                                                                                                                                                                                        .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable siderophore receptor PAl365 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
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C;Superfamily: H+/K+-transporting ATPase chain A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 8, 205-213, 2001
A.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A.Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Experimental source: strain PCC 7120 C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:BA000019; PIDN:BAB75945.1; PID:g17133381; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-561 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Nostoc sp. (Strain PCC 7120)
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AG2336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         potassium-dependent ATPase chain A [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Keywords: carbon-carbon lyase; carboxy-lyase
F;3-263/Domain: orotidine-5'-phosphate decarboxylase homology <OPD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakazaki, N.; Shimpo, S.
NA Res. 8, 205–213, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 ASANNGSGLEGLT--DNSLWWNL 482
         25 TSLSSWKHÖGDWANVSNMTFSNGK-LRVKGI-----YYRNADICSRHRVT---SAG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 LASLILLIHDIVVLIPSATALAYPFSLS-----GISNPSFHG----ISQVVYEYAS 461
                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ICSRHRVTSAGLTLQDLQLWCNL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAILTLSLQLILLLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVKGIYYRNAD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 DRKFADIGNTV----KLQYKGGIYRTSKWADITNAHGVTGAGI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 14.0%;
Local Similarity 39.5%;
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.0%; Score 63.5; DE Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
                                                                                 14.0%; Score 63.5;
28.8%; Pred. No. 44;
                                                             11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Mismatches
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Pred. No. 12;
                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 561;
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                                                           23; Indels
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193 NAAKLVAAGMTLKDL 207
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A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                             A; Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE007869; PIDN:AAK86213.1; PID:g15155314; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; PMID:11743194
A;Accession: D97407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein AGR_C_701 [imported] - Agrobacterium tumefaciens (strain C58, Ce C;Speckes: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C;Accession: D97407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-119 <TIGR>
A;Cross-references: GB:U32838; GB:L42023; NID:g1574497; PIDN:AAC23300.1; PID:g1574505
A;Note: best homolog was a hypothetical protein from Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                        Gene: AGR_C_701
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                                       144 LTMVPSFVHEL-DVSIDT----PEWGRVT-MDISYG-----GIFYALVDVRQIGLTIEKA 192
63 SRHRVTSAGLTLQDL 77
                                                                                                      12 LLLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVKGIYYRNADI-----C 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 IAFGKTPQDIQ-W 113
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16; Conservative 19; Mismatche
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Search completed: December 8, 2002, 19:34:43 Job time : 37.1871 secs

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OM protein - protein search, using sw model
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perfect score:
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3: /cgn2_6/ptodata/1/

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Copyright (c) 1993 - 2002 Compugen Ltd.
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138.199 Million cell updates/sec
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sequence 17, Appl sequence 17, Appl sequence 17, Appl sequence 17, Appl sequence 17, Appl sequence 2, Appl sequence 10, Appl sequence 1, Appli sequence 2, Appli sequence 2, Appli sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 3, Appli sequence 2, Appli sequence 3, Appli sequence 3, Appli sequence 2, Appli sequence 2, Appli

ALIGNMENTS

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US-08-996-139-13
; Sequence 13, Application US/08996139
; Patent No. 6017729
TOPOLOGY: 11;
MOLECULE TYPE:
US-08-996-139-13
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APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Euger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                 TELEFAX: (206)233-0646
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
FRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
FRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 22 DE
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                                                                                                                                                                                            REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                TYPE:
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                                                                                                                                                                                                                  Perkins, Patricia Anne
                                                            amino acid
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                                                                                                                                       (206)233-0644
                                                linear
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                            protein
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RESULT 2 US-08-995-659-13

Patent No. Sequence

624221

GENERAL INFORMATION:

B

232 ATEYLQL 238

δ Б

73 TLQDLQL 79

Matches

Local Similarity

39.7%; 59.7%;

Query Match

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WOLECULE TYPE: protein US-08-995-659-13
                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
APPLICATION 14 OCTOBER 1997
                175 ASSGS---HKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
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LENGTH: 317 amino acids
                                        15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
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APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                           NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: WarasKovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13, Application US/08995659
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                                                                                                      39.7%; Score 180.5; DB 4; Length 317; 59.7%; Pred. No. 3.4e-15;
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                                                                                           18; Indels
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                                                                                   2;
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Sequence 4, Application US/09052521C; Patent No. 6316408; GENERAL INFORMATION:
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                                                      US-09-052-521C-4
                                                                            RESULT 4
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                                                                                                                                                                                                                                                                                                                              US-09-215-649A-13
                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                               Query Match
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US-09-215-649A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/09215649A Patent No. 6271349 GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
                                                                                                                                                                     175 IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
                                                                                                                      232 ATEYLQL 238
                                                                                                                                                         73 TLQDLQL 79
                                                                                                                                                                                        15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
SOFTWARE: MICROSOft WORD FOR POWER MACINTOSH 6.0.1
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: cUnknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappab
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 317 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 98101
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galibert,
                                                                                                                                                                                                                                                       39.7%; Score 180.5; DB 4; Length 317; 59.7%; Pred. No. 3.4e-15;
                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                            18; Indels
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В δÃ

Matches Query Match

40;

Local Similarity

TOPOLOGY:

amino acid OGY: linear

2

APPLICATION NUMBER: FILING DATE: 23 DE CLASSIFICATION:

CLASSIFICATION:

APPLICATION NUMBER: FILING DATE: 22 DE

MEDIUM TYPE;

98101

USA

STREET: COUNTRY:

Seattle

WA

ADDRESSEE:

APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-451Brv

CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 08/880,855 PRIOR FILING DATE: 1997-06-23

PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1997-04-16

08/842,842

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TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-577-780-13
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                                                             MOLECULE TYPE: protein US-08-996-139-11
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                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/
APPLICATION NUMBER: USSN 08/
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/
APPLICATION NUMBER: 199
FILING DATE: 23 DECEMBER 199
ATTORNEY/AGENT INFORMATION:

NAME: PETKINS, PATRICIA Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                              Query Match
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Matches
                 Best
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INFORMATION FOR SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 ATEYLQL 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 28
REFERENCE/TION INFORMATION:
                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                   TELEPHONE:
            Match 38.7%;
Local Similarity 55.4%;
                                                                                                    TOPOLOGY:
                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98101
   36;
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                                                                                                                                                                                                                                                                    Perkins, Patricia Anne
                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: Apple Operating System 7.5.5 Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                   294 amino acids
 Conservative
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                                                                                                      linear
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                                                                                                                                                                                                     (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US/08/996,139
22 DECEMBER 1997
                                                                                                                                                                                                                                                                                                      23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                         14 OCTOBER 1997
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                                                                                                                                                                                                                                             2851-A
        6; Mismatches
                     Score 176; DB 3; Length 294; pred. No. 1.2e-14;
                   2;
                     Gaps
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175 IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231

15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72

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232 ATEYLQL 238

73 TLQDLQL 79

US-09-577-780-13

Sequence 13, Application US/09577780 patent No. 6419929
GENERAL INFORMATION: ADDRESS. Dirk M. APPLICANT: ADDRESS. Dirk M.

CORRESPONDENCE ADDRESS:

COUNTRY: USA STATE: WA CITY: Seattle

ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19

Galibert, Laurent Maraskovsky, Eugene

TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:

LENGTH: 317 amino acids

APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
PPLICATION NUMBER: USSN 08/813,509
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: 1996
ATTORNEY,AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REGERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:

PRIOR APPLICATION DATA:

FILING DATE: 24-May-2000 CLASSIFICATION: <Unknown> APPLICATION NUMBER: US/09/577,780 FILING DATE: 24-May-2000

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 7.5.5
CURRENT APPLICATION DATA:

US-09-052-521C-4

Matches Query Match

Local Similarity es 40; Conserv

Conservative

39.7%; 59.7%;

Score 180.5; DB 4; Length 317; Pred. No. 3.4e-15; 4; Mismatches 18; Indels 5;

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SEQ ID NO 4

LENGTH: 317 TYPE: PRT ORGANISM: Human

NUMBER OF SEQ ID NOS: SOFTWARE: Patentin Ve

PatentIn Ver. 2.1

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US-08-995-659-11
                                                                                                                                  Matches
                                                                                                                                                            Query Match
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US-08-995-659-11
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                                                                                                                                                                                                                                                                           TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO:
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211 BYLOL 215
                                             151 SIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGEYYLYANICERHHETSGSVPT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/08995659 Patent No. 6242213
                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
CRAPHICATION DATA:
PRIOR APPLICATION DATA:
USSN 08/772,330
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                                   75 QDLQL 79
                                                               17 SISHEAHKTSLSSWKHDQDWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                          Local Similarity
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 23 DE
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FILING DATE: 14 OCTOBER 1997
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FILING DATE: 22 DECEMBER 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Apple Operati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Immunea CC-STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 SIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 QDLQL 79
                                                                                                                        36; Conservative
                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                             294 amino acids
                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                               23 DECEMBER 1996
                                                                                                                          38.7%; Score 176; DB 4; Length 294; 55.4%; Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apple Operating System 7.5.5 ft Word for Power Macintosh 6.0.1
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                                                                                                                   Mismatches
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Sequence 11, Application US/09577780
Patent No. 6419929
GENERAL INFORMATION:
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Best Local Similarity
Watches 36; Conserve
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEFAX: (206)587-0430
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-09-215-649A-11

Sequence 11, Application US/09215649A
Parent No. 6271349

The comparison of the comparison o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 SIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLKVNQDGFYYLYANICFRHHETSGSVPT 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 QDLQL 79
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
                                                                                                  APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
Type: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/996,139
FILING DATE: CUNKNOWN:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Galibert, Laurent
Maraskovsky, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.7%;
55.4%;
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                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08842842
Patent No. 5843678
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 11:
                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                            TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 SIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 DYLQL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 SISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jes 36; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 QDLQL 79
                                                                                                                                                                   STREET: 1840 Dehavid
CITY: Thousand Oaks
                                                                                                        ZIP: 91230-1789
                                                                                                                                             STATE: California
  SOFTWARE:
                                                                                                                       COUNTRY:
                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/577,780 FILING DATE: 24-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Immunex Corporation, Law Department
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                                                                                                                                                                                      E: Amgen Inc.
1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                             Boyle, William J.
                                                                                                                            USA
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 176; DB 4; Length 294; Pred. No. 1.2e-14;
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; MOLECULE TYPE: US-08-989-362-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 7:
                                                                                                     TELEFAX: (650)496-1209
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
                                                                                                                                                                                   FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34/
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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CLASSIFICATION: 56
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: you CTIY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 SIPSGSHKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 SISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTL 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                    TYPE:
                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/032,846 FILING DATE: 13-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                      TOPOLOGY:
                                                                   LENGTH:
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                                                  : 316 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                      linear
                protein
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Query Match

38.7%;

Score 176;

DB

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US-09-052-521C-34
                                                                                                                         PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 34
LENGTH: 28
TYPE: PRT
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APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteopro
FILE REFERENCE: A-451Brv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-052-521C-2
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                Sequence 34, Application US/09052521C Patent No. 6316408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30
                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 08/PRIOR FILING DATE: 1997-04-16
                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/PRIOR FILING DATE: 1997-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30 PRIOR APPLICATION NUMBER: 08/880,855
                                                 OTHER INFORMATION: Description of a OTHER INFORMATION: Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Boyle, Willian TITLE OF INVENTION: Oster FILE REFERENCE: A-451Brv
                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
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PRIOR FILING DATE: 1997-04-16
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ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 SIPSGSHKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 DYLQL 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                     ___Osteoprotegerin Binding Proteins and Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1997-06-23
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   Score 76;
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; TYPE: PRT
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5206163-1
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                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09336643A Patent No. 6399761
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. 6399761el Human Potassium Channels FILE REFERENCE: SE0-15p CURRENT APPLICATION NUMBER: US/09/336,643A CURRENT FILING DATE: 1999-06-18 PRIOR APPLICATION NUMBER: 60/076,687 PRIOR FILING DATE: 1998-08-07 PRIOR PILING DATE: 1998-08-07 PRIOR PILING DATE: 1999-01-19 PRIOR APPLICATION NUMBER: 60/116,448 PRIOR FILING DATE: 1999-01-19 PRIOR APPLICATION NUMBER: POT/US99/03826 PRIOR FILING DATE: 1999-02-22 PRIOR FILING DATE: 1999-03-22 PRIOR FILING DATE: 1999-03-23 PRI
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APPLICATION NUMBER: US/07/550,816
FILING DATE: 06-JUL-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: RENARD, ANDRE; DINA, DINO; MARTIAL, JOSEPH TITLE OF INVENTION: DNA ENCODING BOVINE DIARRHEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
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FILING DATE: 29-MAR-1989
APPLICATION NUMBER: 752,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 14.9%; Score 68; DB 6; Length 1286; Local Similarity 23.4%; Pred. No. 6.1;
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Wang, Jian-Wang
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              Conservative
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                                   14.8%; Score 67.5; 22.0%; Pred. No. 2;
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Tue Dec 1, 10:51:39 2002
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perfect score:
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                                                                                                                            Result
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455
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219.722 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Agenesed_101002:*

A. Genesed_101002:*

A. Gene
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Listing first 45 summaries
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AAB68273
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AAW83020
                                  AAW83195
AAW83018
                                            Human PRO protein,
Human PLAG-murine
Mouse RANKL Home
Human PRO206 polyp
Human PRANCE Prote
Human TRANCE Prote
Human Osteoprotege
Human osteoprotege
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OSTEOCLASTOGENESIS
OSTEOCLASTOGENESIS
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25-JUL-2000; 2000US-220585P.
25-JUL-2000; 2000US-220607P.
25-JUL-2000; 2000US-22063P.
25-JUL-2000; 2000US-220638P.
25-JUL-2000; 2000US-220636P.
25-JUL-2000; 2000US-220636P.
25-JUL-2000; 2000US-22083P.
25-JUL-2000; 2000US-22083P.
25-JUL-2000; 2000US-220710.
26-JUL-2000; 2000WS-US20710.
                                                                                                                                                                                                                                                                                                   numan; secreted protein; pRO; tumour; lung cancer; tumour; liver tumour; human; secreted protein tumour; rectal tumour; liver tumour; breast cancer; prostate tumour chondrocyte cell proliferation; pericyte cell proliferation; tumour necrosis factor alpha.
                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                         WO200208288-A2.
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Antibody; OPGbp; Osteopathic; FLAG-murine OPGbp(158-316); bone resorption; loss of bone mass; bone tumour; rheumatoid arthritis; hypercalcaemia of malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides of the PRO polypeptides are useful for diagnostic acids of the PRO polypeptides are useful for diagnosting tumours, especially lunguary the properties are useful for diagnosting tumours, respectively consisteration of, or gene expression, in pericyte cells, for stimulating or inhibiting the prostate tumour, prostate tumour, rectal tumour or fibroblast cells. The PRO polypeptides is for stimulating the release of tumour necrosis for stimulating the release of tumour necrosis for stimulating the release of tumour necrosis factor alpha from human blood, and in chromosome and gene mapping. The PRO polypeptide are not formal human dermal xxx protein sequences of the invention. ANU83592-ANU83713 represent human probes,
                                                                                                                   Mouse FLAG-murine OPGbp[158-316].
                                                                                                                                                                             17-DEC-2001
                                                                                                                                                                                                             AAU08386 standard; Protein; 170 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Figure 82; 359pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              One hundred and twenty two nucleic acids encoding PRO polypeptides, such as lung cancer, colon cancer, breast tumour or liver tumour - colon cancer, breast tumour, prostate tumour, rectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-2000; 2000WO-US23522.
15-SEP-2000; 2000WO-US23528.
10-NOV-2000; 2000WO-US3328.
28-NOV-2000; 2000WO-US30873.
20-DEC-2000; 2000WO-US30646.
20-DEC-2000; 2000WO-US34678.
20-DEC-2000; 2000WO-US34578.
20-DEC-2000; 2000WO-US34568.
20-DEC-2000; 2000WO-US34566.
20-DEC-2000; 2000WO-US34568.
20-DEC-2000; 2000WO-US34568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   84,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABK33576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-172001/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAY-2001;
                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desnoyers L, (
                                                                                                                                                                                                                                                                                                                                                                                   96.7%; Score 440; DB 23; Length 95;
111ve 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-US17092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
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RESULT 3
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                                                                                                                                                                                                                                              Qγ
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Human; Apo2 ligand: divalent metal ions; viral infection; cancer.
                                                                                                                                                                                                                                                                                                            CC The invention relates to an antibody or antigen binding domain or derivative), which binds to an osteopration of derivative), which binds to an osteopration or activation or activation, inhibit be administed antibody.

CC osteoclast formation or activation, inhibit bone resorbind to formation or activation, inhibit bone resorbind to inhibit of separation of secoprocal growth in bone mass in a mammal and to prevent or in a mammal, where loss of bone mass resorbing in a mammal, and to prevent or treat present sequence encodes FLAG-murine OPCDp[158-316].
                                                                           Human RANKL
                                                                                                                                                                                                                                                                                                                                                                                                 18-APR-2001
                                                                                                                           AAB67248;
                                                                                                                        AAB67248 standard; protein; 152 AA.
                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                      87 EYLOL 91
                                                                                                                                                                                                27 SIPSGSHKVTLSSWYHDRGWAKISNWYLSNGKLKVNQDGFYYLYANICFRHHETSGDLAT 86
                                                                                                                                                                                                                17 SISHEAHKTSLSSWKHDODWANVSNWTESNGKLRVK--GIYYENADICSRHKVTSAGLTL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 10; Fig 28; 239pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibodies that bind antagonistically to osteoprotegrin binding bone, rheumatoid arthritis, hypercalcaemia of malignancy and to steoporosis, metastasis of cancer to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS13369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deshpande RV, Hitz A, Boyle WJ, Sullivan JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-FEB-2000; 2000US-0511139.
22-FEB-2001; 2001US-0791153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-FEB-2001; 2001WO-US05973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W0200162932-A1.
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            steroid-induced osteoporosis; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                        39.8%; Score 181; DB 22; Length 17
56.9%; Pred. No. 8.1e-15; Length 17
6; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note wild-type Ser-Val-Pro-Thr-Asp
substituted by Asp-Leu-Ala-Thr-Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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RESULT 4
AAB08273
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                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a formulation comprising Apo-2 ligand and divalent metal ions. Apo-2 ligand and the formulation are useful for treating cancers and viral infections. Addition of divalent metal ions for making Apo-2 ligand and formulations containing Apo-2 ligand results in increased yield and stability of Apo-2 ligand trimers.
                          12-FEB-1999;
18-NOV-1999;
                                                                                                        Homo sapiens.
                                                                                                                       AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease; type II transmembrane protein; B cell stimulatory factor; inflammatory disorder; immune disorder; rheumatoid arthritis; lupus and graft versus host disease.
                                                                                                                                                                                      04-DEC-2000
                                                                                                                                                                                                                      AAB08273 standard; Protein; 160 AA.
                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 3; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of divalent metal ions for making Apo-2 ligand and in formulations containing Apo-2 ligand for increasing yield and stability of ligand trimers, useful for therapeutic applications -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ashkenazi AJ,
O'Connell M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200100832-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
          (AMGE-) AMGEN INC
                                                    11-FEB-2000; 2000WO-US03653
                                                                                       WO200047740-A2
                                                                                                                                                                   Amino acid sequence of a human TNF ligand QPGL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUN-2000; 2000WO-US17579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JAN-2001
                                                                                                                                                                                                                                                                                     73
                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                   70 ATEYLQL 76
                                                                                                                                                                                                                                                                                                                     15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                    TLQDLQL 79
                                                                                                                                                                                                                                                                                                    IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 69
                                                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                           152 AA;
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pai R,
                          99US-0119906
99US-0166271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hymowitz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0141342
                                                                                                                                                                                                                                                                                                                                                 39.7%;
59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shahrokh Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kelley RF, Koumer okh Z, Simmons L;
                                                                                                                                                                                                                                                                                                                                        4.
                                                                                                                                                                                                                                                                                                                                                Score 180.5; DB 2
Pred. No. 8.1e-15;
                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koumenis
                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                       Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leung
                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                               AAU86148
ID AATT
                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
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                                                                                                                                                                                                                                                                                                                              Дb
                                                                                                                                                                                                                                                                                                                                                                                                            Best
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                    Matches
      02-JUN-1999
22-JUN-1999
22-JUN-1999
22-JUL-1999
26-JUL-1999
26-JUL-1999
17-AUG-1999
31-AUG-1999
                                                                          08-MAR-1999;
11-MAR-1999;
11-MAY-1999;
                                                                                                               11-FEB-2000;
                                                                                                                                 26-JUL-2001.
                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                15-JUL-2002
                                                                                                                                                                                                                                                                  AAU86148;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boyle WJ,
                                                                                                                                                  WO200153486-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                             75 ATEYLQL 81
                                                                                                                                                                                                                                                                                                                                               73 TLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                     160 AA;
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                                                                    -Sn66
-Sn66
-Sn66
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AABO8265-83 represent tumour necrosis factor (TNF) ligands. The specification describes an AGP-3 polypeptide, which is TNF ligand family member. AGP-3 is a type II transmembrane protein, and is a potent B cell stimulatory factor. Expression of AGP-3 correlates to increases in the number of B cells and immunoglobulins produced. AGP-3 proteins, antibodies, and nucleic acids may be used to treat inflammatory and immune disorders, e.g. rheumatoid arthritis, Crohn's disease, lupus and graft versus host disease. The nucleic acids may be used to regulate the expression of an AGP-3 related protein. The AGP-3 proteins, antibodies and nucleic ands are also useful for the detection of AGP-3 agonists, antagonists and characterizing interactions with AGP-3 related proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disoinflammatory disorder; immune disorder; angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 14; Fig 9; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides comprising tumour necrosis factor ligand family proteins, useful for treating inflammatory and immune disorders, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PRO206 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU86148 standard; Protein; 244 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US03565
99US-140650P.
99US-140653P.
99US-144758P.
99US-145698P.
99US-146222P.
99US-149395P.
99US-151689P.
                                                                                                                                                                                                                                                                                                                99WO-US05028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.7%;
59.7%;
                                                                                                                                                                                                                                                      -133459P.
                                                                                                                                                                                                                                                                                      123972P
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Pred. No. 8.7e-15;
4; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.g.
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RESULT 6
AAU78286
         ID XXX ACC XXX
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Best Local :
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30-NOV-1999;
01-DEC-1999;
01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and anglogenic disorders. The polynucleotide sequences are also useful in gene therapy. AAU86128-AAU86162 represent the human PRO
                                                                                                                                                                                                        TRANCE: dwarfism; osteopetrosis; craniofacial-skeletal discrepancy; bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis; rheumatoid arthritis; arcomegaly; gigantism; exostosis; carilaginea; exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte; exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thirty five nucleic acids encoding PRO polypeptides, useful fitreating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disord
18-Aug-2000; 2000US-226197P
                                        20-AUG-2001; 2001WO-US26101.
                                                                                                                     WO200216551-A2
                                                                                                                                                        Homo sapiens
                                                                                                                                                                                           cartilage growth;
                                                                                                                                                                                                                                                                                                                        Human TRANCE protein splice variant
                                                                                                                                                                                                                                                                                                                                                                 18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU78286 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 61; Fig 42; 302pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
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Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATEYLQL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLQDLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-205567/26.
                                                                                                                                                                                                                                                                                  tumour necrosis factor-related activation induced cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK40274.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan J, | Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US21090.
99WO-US28313.
99WO-US28301.
99WO-US28634.
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an J, Pitti RM,
                                                                                                                                                                                           skeletal growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.7%;
59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Godowski PJ,
i RM, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 180.5; DB 2
Pred. No. 1.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gurney
Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
 02-DEC-1997;
15-APR-1997;
09-JUN-1997;
                                                                                                                                                      WO9846644-A1
                                                                                                                                                                                                                                                              Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
                                                                                                                                                                                                                                                                                                   Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
                                                                                                                                                                                                                                                                                                                                                                                                                   AAW83020 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                             15-APR-1998;
                                                                                                                 22-0CT-1998
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                               osteoclast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATEYLOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLODLOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPSGS----HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-304119/34.
DB; ABK12877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 40; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fig 4; 55pp; English.
                                                                                                                                                                                                                                             bone absorption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79
 97JP-0332241.
97JP-0097808.
97JP-0151434.
                                                                             98WO-JP01728
                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.7%;
59.7%;
                                                                                                                                                                                                                                               factor; bone disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                   246
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calcium metabolism;

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resulting from traumatic injury, surgery, osteoarthritis or rheumatoid arthritis, and disorders comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, carilaginea, exostosis bursata and multiple osteocartilaginous exostoses. The method is useful for inhibiting chondrocyted differentiation. The present amino acid sequence represents the human TRANCE protein, splice variant 2 of the invention. TRANCE is a member of the tumour necrosis factor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a new method of treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth. The method of the invention involves administering to the mammal a tumour necrosis factor-related activation induced cytokine (TRANCE)-modulating agent. The method is useful for treating a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating mammal having disorder characterised by abnormal cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor-related activation induced cytokine-modulating agent to mammal
                                                                                                                                                                                                                                                                                                                                                                                              and acts directly on cartilage-producing cells (chondrocytes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or skeletal growth is selected from dwarfism, osteopetrosis, craniofacial-skeletal discrepancies and bone or cartilage damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     having a disorder comprising insufficient or excessive cartilage or skeletal growth, where the disorder comprising insufficient cartilage
IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNIV MASSACHUSETTS MEDICAL CENT.
                                                                                           Score 180.5; DB Pred. No. 1.5e-14
4; Mismatches 1
                                                                                                                                                                                            23;
                                                                                                Indels
                                                                                           <u>ن</u>
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                                                                                                                                                                                                                                                                                                                                      RESULT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (sOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic nurrous.
 30-MAR-1998;
16-APR-1997;
                                                                                                                          Homo sapiens
                                                                                                                                                                   hypercalcaemia;
                                                                                                                                                                                Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
                                                                                                                                                                                                                       Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.
                                                                                                                                                                                                                                                     11-FEB-1999
                                                                                                                                                                                                                                                                                                          AAW83195 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          components
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents an osteoclastogenesis inhibitory (OCIF)-binding molecule (OBM). The protein promotes and supports separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 28; Pages 119-120; 151pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-594563/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-AUG-1997;
21-AUG-1997;
                                         15-APR-1998;
                                                                     22-OCT-1998
                                                                                                                                                      Paget's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakagawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SNOW ) SNOW BRAND MILK PROD CO
                                                                                                                                                                                                                                                                                                                                                                              161 ATEYLQL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                    104
                                                                                                                                                                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                                                                                              15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                        TLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                 IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. treatmen
.um metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
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a N, Shima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97JP-0217897.
97JP-0224803.
98US-0052521
97US-0842842
                                         98WO-US07584
                                                                                                                                                                   osteoclast differentiation
                                                                                                                                                                                                                                                                                                            Protein; 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kinosaki M,
Takahashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 180.5; DB 1
Pred. No. 1.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kobayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomoyasu
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Þ, 4
                                                                                                                                                                   activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morinaga
Tsuda E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor
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RESULT 9
AAW83018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is human osteoprotegerin (OPG) binding protein.
CC Host cells transfected with vectors containing nucleic acid molecules
CC encoding OPG binding protein are used to produce recombinant OPG binding
CC protein. OPG binding protein is used in binding assays to determine
CC protein. OPG binding protein is used in binding assays to determine
CC binding agents (particularly agonists and antagonists, including
CC intracellular proteins); to raise Ab (useful in immunoassays for
CC detection of OPG binding protein) and to identify compounds that
CC modulate binding of OPG binding protein to scheoclast differentiation
CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC binding protein can be used to detect OPG binding protein-encoding
CC sequences, e.g. screening for related sequences, also to produce
CC transgenic animal models, while complementary sequences are used for
CC off binding protein, particularly soluble forms of OPG binding protein
CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
CC disease, periodontal disease, osteoporosis, loosening of prostheses,
CC disease, periodontal disease, osteoporosis, loosening of prostheses,
CC optionally in combination with agents that promote bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                        Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 19; Fig 4; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-1997;
                                                                 22-OCT-1998.
                                                                                                  W09846644-A1
                                                                                                                                    Homo sapiens
                                                                                                                                                                                       osteoclast;
                                                                                                                                                                                                         Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
                                                                                                                                                                                                                                                                              10-FEB-1999
                                                                                                                                                                                                                                                                                                                                                AAW83018 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-594578/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                       232 ATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 IPSISHEAHKTSLSSWKHDQDWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 TLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317
                                                                                                                                                                                         bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97us-0880855.
                                                                                                                                                                                       absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                  Protein; 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.7%;
59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 180.5; DB 1
Pred. No. 2.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 317;
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02-DEC-1997; 15-APR-1998;

98WO-JP01728

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AAW69957
ID AAW69957
AC AAW69

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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09-JUN-1997;
12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (gOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as
14-OCT-1997;
                                                                22-DEC-1997;
                                                                                                                     02-JUL-1998.
                                                                                                                                                                           W09828426-A2
                                                                                                                                                                                                                                                                                                         RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                          NF-kB receptor activator RANK ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW69957 standard; Protein; 317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 36; Pages 113-114; 151pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and calcium metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-594563/50.
N-PSDB; AAV69887.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakagawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SNOW)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 ATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 TLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                  RANK ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNOW BRAND MILK PROD CO
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N, Shima N,
N, Yamaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97JP-0097808.
97JP-0151434.
97JP-0217897.
97JP-0224803.
           97US-0064671
                                                                97WO-US23775
                                                                                                                                                                                                                                                                                  tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.78;
59.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinosaki M,
Takahashi K,
i K, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 180.5; DB 1
Pred. No. 2.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kobayashi
(, Tomoyasu
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                          (RANKL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Þ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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Tsuda E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-KB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of can also be used to identify inhibitors of RANK and thus inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This represents a human RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappaB (NF-kB) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. A soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds tRANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their
                                   02-JUL-1998.
                                                                    WO9828424-A2
                                                                                                                                         RANK; necrosis factor-kappa B; NF-kB; receptor activator; immune response; inflammatory response; toxic shock; seps RANKL; RANK ligand; tumour necrosis factor; TNF.
                                                                                                                                                                                                                NF-kB receptor activator RANK ligand
                                                                                                                                                                                                                                                     08-OCT-1998
                                                                                                                                                                                                                                                                                                                        AAW68293 standard; Protein; 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of TNF-alpha. The products can also be used for detection and drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; Pages 59-60; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated ligand for receptor activator of NF-kappa develop products for augmenting an immune response for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory response and for protection of cells
                                                                                                                                                                                                                                                                                                                                                                                                                 232 ATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 TLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
40; Conserv
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                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
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97US-0813509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.7%;
59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maraskovsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 180.5;
Pred. No. 2.1
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                                                                                                                                                                                                                (RANKL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B - used to inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used to
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22-DEC-1997;

97WO-US23866.

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. Host cells transformed or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for alsease characterised by neoplastic cells that express RANK. The products
               Region
                                               Domain
                                                                                                                          Homo sapiens
                                                                                                                                                                   tumour necrosis factor receptor; type II transmembrane protein;
osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                                                                                                   Osteoprotegerin ligand; OPGL; osteoprotegerin;
                                                                                                                                                                                                                               Amino acid sequence of a human osteoprotegerin ligand (OPGL).
                                                                                                                                                                                                                                                               25-JUL-2000
                                                                                                                                                                                                                                                                                                                        AAY84417 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMV ) IMMUNEX CORP.
                                                                            Region
                                                                                                                                                        1mmune
                                                                                                                                                                                                                                                                                                                                                                                                     232 ATEYLQL 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isolated receptor activator of necrosis factor-kappa B - useful, e.g. developing products for regulating an immune or lammatory response, treating toxic shock or sepsis
                                                                                                                                                                                                                                                                                                                                                                                                                                 TLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represents a human RANKL, a ligand for the RANK (receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPSGS----HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
                                                                                                                                                      response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Pages 59-60; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be used for detection and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Galibert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0064671.
96US-0059978.
97US-0813509.
                                                                            Location/Qualifiers 49..69
                 /note= "extracellular stalk domain"
158..317
                                                 70..157
                                                             /note=
                                                                                                                                                     osteoporosis; bone resorption.
                                                                                                                                                                                                                                                                                                                        Protein; 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ĽĮ,
                                                            "transmembrane region"
"active ligand moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180.5; DB 1
No. 2.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19;
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                                                                                                                                                                                                 osteoclastogenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317;
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                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                                                                  AAE08738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a human osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                                                                                                                                      Human receptor activator of NF kappaB ligand (RANKL) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 19; Page 78-79; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to treat,
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                               US6271349-B1
                                                            Homo sapiens
                                                                                           anti-apoptotic
                                                                                                       toxic shock;
                                                                                                                                        Human; receptor activator of nuclear factor kappaB ligand; tumour necrosis factor; TNF; TNF receptor associated factor
                                                                                                                                                                                                                       15-NOV-2001
                                                                                                                                                                                                                                                                                   AAE08738 standard; Protein; 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halkier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MEBI-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000.
                                                                                                       immune response; inflammatory response; graft-versus-host reaction; toxic shock; sepsis; acute inflammatory reaction; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                            175 IPSGS---HKYSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL
                                                                                                                                                                                                                                                                                                                                                                 232 ATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                              73 TLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-271444/23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        down-regulation of osteoprotegerin ligand (OPGL) activity used t, prevent and ameliorate osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                     (first entry)
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98US-0102896
                                                                                          signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-DK00481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.7%;
                                                                                          therapy; immunosuppressant; anti-inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 180.5; DB 2
Pred. No. 2.1e-14;
                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 317;
                                                                                                                                           factor;
                                                                                                                                                          RANKL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                       CC are useful for regulating immune response and in screening for inhibitors CC of these receptors. The cytoplasmic domain of RANK is used in developing CS assays for inhibitors of signal transduction, e.g. for screening the CC molecules that inhibit interaction of RANK with TRAFI TRAF2, TRAF3, CC TRAF5 and particularly TRAF6. NF kappaB inhibition by RANK antagonists CC are useful in ameliorating the negative effects of an inflammatory CC response that result from triggering of RANK, e.g. in treating toxic reactions and the effects of bone resorption. RANK acts as an anti-CC shock or sepsis, graff-versus-host reactions, acute inflammatory CC reactions and the effects of bone resorption. RANK acts as an anti-CC soluble forms of the receptor are used in vivo or in vitro based CC screening tests for agonists of antagonists of RANK activity, as CC antagonists of RANK-mediated NF-kappa B activation, or to inhibit CC transduction of a signal via RANK. RANK compositions are used in the CC development of both agonistic and antagonistic antibodies, or as an CC adjunct therapy for disease characterised by neoplastic cells that CC express RANK. Compounds that interfere with RANK/TRAF6 interactions CC are useful for modulating osteoclast function and activities. They care useful for the expression of recombinant proteins, as probes for analysis of the presence or distribution of RANK transcripts, while the proteins CC are useful in preparing kits for the detection of soluble RANK, or CC monitor RANK-related activity. The present sequence is RANK ligand CC (RANKL) protein from human.
                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The patent discloses novel receptor activator of nuclear factor (NF)-
kappaB (RANK) proteins and their corresponding DNAs. RANK is a member
of the tumour necrosis factor (TNF) receptor superfamily and associates
with TNF receptor associated factor (TRAF) 2 and 3 which are important
in the regulation of immune and inflammatory response. The receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as adjunct therapy for disease characterized by neoplastic cells that express RANK
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                              (RANKL) protein from human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The patent discloses novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 15; Column 71-72; 47pp; English
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07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1996;
07-MAR-1997;
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                                                                                        232 ATEYLQL 238
                                                                                                                                                                                                15 IPSISHEAHKTSLSSWKHDQDWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                73 TLQDLQL
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                                                                                                                                                                         IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 23:
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                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         970S-0064671.
960S-0772330.
970S-0813509.
970S-0996139.
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59.7%;
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Pred. No. 2.1e
4; Mismatches
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AAE01993
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Best Local
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07-MAR-1997;
14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to receptor activator of NF-chi B (RANK) DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2 and TRAF3. The DNA molecules are useful for producing ligands of RANK. The ligands are useful for regulating immune response and in screening for inhibitors of RANK. The present sequence is human RANKL (hurankkl)
               AAE01993;
                                                             AAE01993 standard; Protein; 317
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi | receptor activator) of the receptor activator of NF-chi B (RANK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; receptor activator of NF-chi B; RANK; tumour necrosis factor; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-407216/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson DM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human receptor activator of NF-chi B ligand (huRANKL) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE04426 standard; Protein; 317
                                                                                                                                                                                                                                                             175
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                                                                                                                                                                     232 ATEYLQL
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                                                                                                                                                                                                                73 TLQDLQL 79
                                                                                                                                                                                                                                                        IPSGS----HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
                                                                                                                                                                                                                                                                                                                                                   40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Column 65-66; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    317 AA;
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97US-0077181.
97US-0064671.
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59.7%;
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Pred. No. 2.1e-14;
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317; 5; Gaps

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                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a novel receptor, referred to as RANK CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF CC (tumour necrosis factor) receptor superfamily. RANK is a Type I CC transmembrane protein that interacts with TNF receptor-associated CC factors (TRAFs). Triggering of RANK by overexpression or co-expression of RANK and membrane bound RANK ligand (RANKL) results in upregulation of factor (TRAFs). Triggering of RANK by overexpression or co-expression of that is most extensively utilised in cells of the immune system.

CC Inhibition of Nf-kappaB by RANK antagonists is useful in ameliorating consertive effects of inflammatory reactions, and the effects of excess bone resorption. The RANK DNAs, proteins and their analogues are useful for the preparation of pharmaceutical compositions, for infecting target cells for use in gene therapy applications in diagnosing diseases associated with RANK, and as targets for use in screening assays. They may be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct consecutivating mutations, associated with e.g. familial expansile costeolysis (FEO) and early onset Paget's disease of bone (EP). The present amino acid sequence is full-length human RANKL (huRANKL) correct protein. The RANKL gene is located in chromosome 13q14.
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB; NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic; inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial expansile osteolysis; FEO; early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14.
                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 76-77; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA encoding a receptor activator of NF-kappaB polypeptide for the treatment of Paget's disease and Familial Expansile Osteolysis (FEO) - \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human full-length RANKL (receptor activator of NF-kappaB ligand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2001 (first entry)
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                                                                                 232 ATEYLOL 238
                                                                                                                                                                                15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                     73 TLQDLQL 79
                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                             IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
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59.7%;
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                                                                                                                                                                                                                                            Score 180.5; DB 2
Pred. No. 2.1e-14;
4; Mismatches 18
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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204
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Copyright (c) 1993 - 2002 Compugen Ltd.
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666666	0000000	A1896022 ESTA05405 AL313728 Tetracdon AA1188893 zp79all.r AW750034 PM2-BT054 AW750046 PM2-BT054 AW959012 EST371082 B1260179 602970221 BM836932 K-EST0712 BM836932 K-EST0712 AW958677 EST370747 AW814742 MR1-ST020 AQ013309 RPCII1-23	BF936674 MR2-NT013 BF936674 D2240058 BF683775 602140058 AU226504 AU226504 AU226504 BU226504 BJ445420 BJ445420 AW784685 Zb77808-9	

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RESULT 1
AG107545
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Pan troglodytes DNA, clone: PTB-112G09.F, genomic survey sequence.
AG107545
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Vokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, CE-mail:chimpbes@gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, CE-mail:chimpbes@gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, CE-mail:chimpbes@gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-112609.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 659)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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SOURCE

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Match Length Query

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AG107545 Pan trogl BH267783 CH230-186 AV653073 AV653073 AL768846 Arabidops AA310614 EST181461

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clone tracking errors.

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            410 CCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGGCCAAGATCTCCCAACA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 CTCATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCAL
                                                           Seq primer: T7
Class: BAC ends.
                                                                                                                         Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources
                                                                               (http://www.chori.org/bacpac/or ering_information.htm), BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html plate: 186 row: C column: 1
                                                                                                                                                                                                         9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: Szhao@tigr.org
                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                   Other_GSSs: CH230-186C1.TJ
                                                                                                                                                                                                                                                                                                                    Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134; Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH267783.1 GI:17180093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CH230-186C1 TV CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-186C1, DNA sequence
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Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., (P. and Fraser,C.M.
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R.Site 2
/organism="Rattus norvegicus"
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                             Location/Qualifiers
1. .612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="lymphoblast"
/clone_llb="PTB Chimpanzee Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Clone="PTB-112G09.F"
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74.98;
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Pred. No. 3
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AV653073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            531 TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                    Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                 This clone is available at CHGC in Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                            hanzg@chgc.sh.cn
                                                                                                                       /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
                                                                /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                         /lab_host="SOLR"
                                                                                                                                                              /clone_lib="GLC"
                                                                                                                                                                                /clone="GLCDHB01"
                                                                                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                         Location/Qualifiers
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/Cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: ECORI; Site_2: ECORI;
CHORI-320 Rat (BM/SSNHSd/MCW) BAC library produced by
Pleter de Jong"
145 c 133 g 166 t
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/db_xref="taxon:10116"
/clone="CH230-186C1"
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71.3%; Pred. No. 1.6e-18;
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Score 46.2;

DB 10; Length 362;

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGNGTTGGGCCAAGATCTC 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone MCL19. The sequences are generated at the MPI for Plant Breeding Research in the context of the Gabl-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:

http://www.mpiz-koeln.mgg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana T-DNA flanking sequence GK-079D11-011917,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for flanking sequence tag based reverse genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                              D
                                                                                                                                                                        /clone_lib="Arabidopsis thaliana T-DNA insertion lines" note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were
                                                                                                              removed"
a 37 c
                                                                                                                                                            processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:3702"
/clone="GK-079D11-011917"
                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Arabidopsis thaliana"/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzpegrald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Grehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P. S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmarros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., He, M.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P. J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
                                                  11 ATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCCAAACGTCTCCAACATGA 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               index (http://www.tigr.org/tdb/hgi/hgi.html)
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                                                                                                                                                                                                                                                                                              /clone_lib="Jurkat T-cells V"
/clone_lib="T-lymphocyte"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                          /db_xref="ATCC (inhost):156679"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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 Mismatches

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                                                                                     122 ACATTTGCTCTCGA 135
                                                                                                                                    490 CCAGAAAGACATACATGGATGGTATGCACTCATTGATAAGTGGCTATTAGCCCCAAATGCT 549
                                                           550 TGAATTACTCTAGA 563
                                                                                                                                                                                                                            62 CCAACATGACTTTCAGGAACGGAAAACTAAGAGTCAAAGGCATTTATTATCAGGAATGCCG 121
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                      2 ATGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 NTTNAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATNGGCAGAAATT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 CTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTATCCCGGAATGCCGACATT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhaoetigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 99 row: C column: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat BAC End Sequences from Library CHORI-230 EcoRI segment. Unpublished (1999) Other GSSs: CH230-99C2.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., of Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CH230-99C2.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-99C2, DNA sequence.
BH314331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH314331.1 GI:17244682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 a
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by Pieter de Jong"
190 c 184 g 177 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/strain="BN/SSNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-99C2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="CHORI-230 Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 853
                                                                                                                                                                                                                                                                                                                                                   16.3%;
53.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type="Brain"
                                                                                                                                                                                                                                                                                                                    Score 33.2; DB 17; Length 853; Pred. No. 1.8; 0; Mismatches 63; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                         184 g
                                                                                                                                                                                                                                                                                                                                                                                                                                         177 t
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                RESULT 8
AV979271
                                                                                                                                                                                                                            В
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KEYWORDS
                                             ACCESSION
                                                                                     DEFINITION
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AW750032
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                                                                                                                                                                                                                          318
                                                                                                                                                                                                                                                                                            258 AAACAACGAGCCAAGCTCCAGAAAATGCTGCCCAAGCTGGAAGAAGTTGAAGGCACGA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                               71 CTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATT 126
                                                                                                                                                                                                                                                                                                                                       11 ATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCCAAACGTCTCCAACATGA 70
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                       ATTGAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATGGGCAGACATT 373
                                        AV979271
AV979271 Nori Satoh unpublished cDNA library, egg Ciona intestinalis cDNA clone cieg52120 5', mRNA sequence.
           AV979271
AV979271.1 GI:19468995
                                                                                                                                                                                                                                                                                                                                                                                                     64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-BT0546-
120100-001-a08&t3=2000-01-12&t4=1)
Seg primer: puc 18 forward
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., Bardin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW750032 407 bp mrNA linear EST 28-APR-200 PM2-BT0546-120100-001-a08 BT0546 Homo sapiens cDNA, mrNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW750032.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Onte-Torgan: breast; Vector: pucl8; Site_1: SmaI, Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone_lib="BT0546"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 32.8; DE Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              52;
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REFERENCE
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                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                   AUTHORS
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             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 AAGACCAAGAGAAAGCTTCGTATGCTTA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 TTAATAACACGGAGACATTAGGGAGAAAGGCATCCCACACCTCTCTGATGTCATCGTTTG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 TCAAACCAGCACCTGCGTTGGTTAAACTCAAGAAACTTGAGAAATCGGCACCACTGGGAC 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 TAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGAC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 TTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATTTGCTC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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Ciona intestinalis

Elikaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 561)

Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.

Expressed genes in Ciona intestinalis

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kyoto University Sakyo-ku, Kyoto, Kyoto 606-8502, Japan Tel: 81-75-753-4081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Nori Satoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Zoology
                                                                                                                                                                                                                                                                                                       Brassica oleracea
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 724)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BH671765 724 bp DNA linear GSS 19-FEB-2002
BOMKY36TR BO_2_3_KB Brassica oleracea genomic clone BOMKY36, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BH671765.1 GI:18736884
                                                                                                                                                                                                                                                                                 Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                Brassica oleracea.
                                                                                                                                                                                                                                              Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                        Seq primer: TR
Class: sheared ends.
                                                                                                                                                                                                                        Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81-75-705-1113
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                                                                                                                                       301-838-3523
301-838-0208
                                                                                                                                                                              Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           satoh@ascidian.zool.kyoto-u.ac.jp.
                                                                                                from a doubled haploid provided by
                                                                                                                        cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:7719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="cieg52120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Ciona intestinalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK"
127 c 127 g 157 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Nori Satoh unpublished cDNA library, egg"
/tissue_type="whole animal"
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                                Location/Qualifiers
/organism="Brassica oleracea"
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51.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  628 TAATACATAATAATGAGAAGAATCCATCTACTAGGAAAAGGAAAGGGTTTCATTTTCTCC 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCT 164
                                                                                                                            source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CATGAGGCTCATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTC 60
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                                                                                                                                                                                                                                                                                                                                                                                          Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL350754.1 GI:8244524
                                                                                                                                                               This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                       Charaterization and repeat analysis of the compact genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                   Submitted (12-APR-2000)
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          185
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
a 144 c 162 g 192 t
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                                                              /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="004K23"
/clone_lib="B"
/note="Genoscope sequence ID : C0AB004AF12B1~end : SP6"
/note="Genoscope sequence ID : C0AB004AF12B1~end : SP6"
/note="Genoscope sequence ID : C0AB004AF12B1~end : SP6"
                                                                                                                                                Location/Qualifiers
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                                                                       628 TTTTTTTAGTTTGGAAAAGTAAATCTGAAAGAAGTAAATTCATTTAATCAATACATCAG 569
                                                                                                                                           688 TCAAAAATAAAGTTTTATTTTTGTAAAAACTGTATAACTTTGGAACAAAGTNTAAAACAA 629
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                                                                                                        69 GACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATTTG 128
                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              671 CTTGACACCGTGGAGGNTGAGAAGACANCAACCANCAGCNCAACCNACAAAGGTGAAACA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 CTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTATGGTGTAATT 190
                                                                                                                                                                            9 TCATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACAT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 TGAGA 195
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                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAMI12870 row: k column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1027)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGENCOURT_6808690 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5784700 BQ050697
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                                                                                                                                                                                                                                                                                         /tissue_type="leiomyosarcoma"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
233 c 214 g 292 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:5784700"
                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NIH_MGC_71"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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319 AGTGCAGGCCTTA 331
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                                                                                                                                                                                                                                                                                     199 TTTTGTAAAGATAAAGAAGATTGAACAATCCTCAGCCAAACTAATCAAGGGAAAGAGAAG 258
                                                                                                                                                             148 TCAGCAGGCCTAA 160
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                                                                                                                                                                                                                                                                                                                                28 TCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAA 87
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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Other_GSSs: RPCI-24-64B19.TV
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Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
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Mouse BAC End Sequences from Library RPCI-24
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/strain="C57BL/60"
/db_xref="taxon:10090"
/clone="RPCI-24-64B19"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Cell_type="Spleen/Brain"
/Cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
Library was cloned in the pTARBAC1 cloning vector at the
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                                                                                                                                                                                                                                                                                                                 61 TCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCAT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-NT0135-
131200-014-g01&t3=2000-12-13&t4-1)
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Ludwig Institute for Cancer Research
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                                                                                                     mRNA sequence.
BF683775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/db_xref="taxon:9606"
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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                         Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishi,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AU226504 RAFL14 Arabidopsis thaliana cDNA clone RAFL14-39-G24 3',
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                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 428)
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Large scale analysis of Arabidopsis full-length cDNA
                                                                                                                                                                                                                                                                            Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 912)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: uterus; Vector: pOTH7; Site_1: XhOI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp fol average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:4301127"
/clone_lib="NIH_MGC_46"
/tissue_type="leiomyosarcoma_cell_line"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
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50.0%;
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Pred. No. 4.8;
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Search completed: December Job time: 459.782 secs
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ORIGIN
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Best Local Similarity
Matches 63; Conserv
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                                                                               76 CAGAAGAGAATATCTCAGAGTTTAAGGAAAATATTAACTCATTTACGATTGTTC 130
                                                                                                         75 CAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCCGACATTTGC 129
                                                                                                                                                                     15 AACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGACTTT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9660
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.
                                                                                                                                                                                                                                                                                                                                                                                 140
                                                                                                                                                                                                                                                                 15.6%;
ilarity 54.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAFL14"39-G24"
/clone_lib="RAFL14"
                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="root"
/lab_host="DH10B"
/note="Site_1: BanHI; Site_2: SalI"
/note="Site_1: BanHI; Site_2: SalI"
/note="Site_1: SalI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                     8, 2002, 19:27:16
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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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400100
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                              Match
                                                                                                                                                                                                                 Query
                                                                                                                                                                                                                                                                                                                                                                                //IDS2/gcgdata/geneseq/geneseqn-embl/NA199.DAT:*
SIDS2/gcgdata/geneseq/geneseqn-embl/NA199.DAT:*
SIDS2/gcgdata/geneseq/geneseqn-embl/NA200.DAT:*
SIDS2/gcgdata/geneseq/geneseqn-embl/NA200.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
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  1186
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                                                            AAV41378
AAV41372
AAD15311
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AAD05904
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7908.746 Million cell updates/sec
                         NF-kB receptor act
NF-kB receptor act
Human receptor act
Human receptor act
Human full-length
                                                                                                                                                                                                           Description
                                                                                                                           cDNA encoding huma
Nucleic acid encod
Nucleic acid encod
              encoding huma
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	96.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4	
	155.333333344477.33339.6666666666666666666666666666666	
	22271 22271 22271 1823 951 951 951 951 951 951 951 1630 1630 1630 1630 1630 1630 1630 163	
	224 224 221 221 221 221 221 221 221 221	
ALIGNMENTS	ABK12876 AAZ99964 AAV70285 AAK80223 AAF86481 AAX69988 AAV69900 AAA39156 AAX29995 AAX49996 AAX69886 AAV41377 AAV41371 AAD15903 AAAD5907 AAX60224 AAX99975 AAX99976 AAX99977 AAX29977 AAX441414	
	DNA encoding a human bna encoding human transce economing human human transce encoding human human transce encoding human human transce encoding encoding nucleotide sequence whouse obstaclast formation nucleotide sequence where encoding a murical encoding a murical encoding a murical encoding encoding encoding receptor act whiring receptor act murine receptor act murine receptor act murine rankKL (recemous obstacle) in uncleotide sequence mouse obstacle encocing muleotide in uncleotide sequence mouse obstacle encoding muse human osteoprotege bna encoding osteo bna encoding colo duman cytokinesis	anna encoding huma

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RESULT 1
ABK33576
ABK33576 standard; cDNA; 1186 BP.
                   20-JUL-2000;
25-JUL-2000;
25-JUL-2000;
25-JUL-2000;
25-JUL-2000;
25-JUL-2000;
25-JUL-2000;
                                                                                                                                                                                                Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha; gene; SS.
                                                                                                                                                                                                                                                      CDNA encoding human PRO protein, Seq ID No 81.
                                                                                                                                                                                                                                                                               08-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                   ABK33576;
                                                                                                                                                                              Homo sapiens.
                                                                                                             29-JUN-2001; 2001WO-US21066
                                                                                                                                 31-JAN-2002
                                                                                                                                                        WO200208288-A2.
25-JUL-2000;
26-JUL-2000;
                                ; 2000US-219556P.
; 2000US-220585P.
; 2000US-220605P.
; 2000US-220607P.
; 2000US-220624P.
; 2000US-220638P.
2000US-220664P.
2000US-220666P.
2000US-220893P.
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AAV69899
                                                  RESULT 2
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                                                                                                                                                                                                                                                                                                                                     CC The invention relates to one hundred and twenty two nucleic acids CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides CC encode human secreted proteins. The PRO nucleic acids, polypeptides, CC The PRO polypeptides are useful for treating a PRO related disorder. CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or CC civer tumour. The PRO polypeptides are useful for stimulating the CC the proliferation of, or gene expression, in pericyte cells, for stimulating the CC the proliferation or differentiation of chondrocyte cells, for CC concern the PRO polypeptides are useful for stimulating the CC the proliferation or differentiation of chondrocyte cells, for CC containing the release of tumour necrosis factor alpha from human blood, CC contains the PRO polypeptide may also be used as molecular cCC dibroblast cells. The PRO polypeptide may also be used as molecular cCC applications in molecular biology, including use as hybridisation probes, CCC end in chromosome and gene mapping. ABK33536-ABK33657 represent human cCC contains and for tissue typing. The PRO nucleic acids have cCC and in chromosome and gene mapping. ABK33536-ABK33657 represent human cCC contains coding sequences of the invention.
                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                   Matches 194;
AAV69899;
              AAV69899 standard; cDNA to mRNA; 741 BP.
                                                                                 684 TGGTGTAATTTGAG 697
                                                                                             181 TGGTGTAATTTGAG 194
                                                                                                                    Sequence 1186 BP; 314 A; 285 C; 299 G; 288 T; 0 other;
                                                                                                                                                                       564 TCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCC
                                                                                                                                                                                                                    504 CÁTGAGGCTCATÁAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTC 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour.
                                                                                                                                                                                            61 TCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Figure 81; 359pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                 1 CATGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTC 60
                                                                                                                                                                                                                                                                                                 Local
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15-SEP-2000;
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                                                                                                                                                                                                                                                                                             Similarity
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C, Gurney AL,
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2000WO-US32678
2000US-0747259
2000WO-US34956
2001WO-US06520
2001WO-US06520
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2000WO-US23522.
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2000WO-US30873.
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                                                                                                                                                                                                                                                                                    95.1%; Score 194; DB 24; Length 1186; 100.0%; Pred. No. 2e-57;
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Smith V, Stephan JF,
                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                        0; Indels
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محمد CK, Wood WI;
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                                                                                                                                                                                                                                                                   Gaps
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                                       Qγ
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                                                                                                             Matches 137;
                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
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Washida N, Yamaguchi K,
                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-1997;
12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-1997;
15-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1998-594563/50.
                                                                                                                       Similarity
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                                                                                                          Conservative
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97JP-0097808.
97JP-0151434.
97JP-0217897.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1..741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kinosaki M, Kobaj...
i, Takahashi K, Tomoyası
                                                                                                      0; Mismatches
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117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 741 BP; 230 A; 153 C; 158 G; 200 T; 0 other;
                                                                                              378 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone
                                                                                                                                                                                                                           318 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and
                                                                                                                                                              63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding a human OCIF-binding molecule (OBM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                                                          47.3%; Score 96.4; DB 19; Length 741; 74.5%; Pred. No. 2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kobayashi F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tomoyasu A,
                                                                                                                                                                                                                                                                                                                                                               41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morinaga T;
, Tsuda E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV69887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding a human OCIF-binding molecule (OBM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV69887 standard; cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osteoclast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 GCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9846644-A1
                                                                                   corp. -binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). absorption factor by separation and solubilisation of membrane proteins absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence then affinity chromatography which is a shorter chain. OBM may be form and a solubilised form (soBM) which is a shorter chain. OBM may be used for screening for receptors to OBM which mediate its function. activity, and screening for receptors to OBM which mediate its function these substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the navier of the content of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakagawa N, Shima M, Amerika Nano K, Washida N, Yamaguchi K, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-1997;
15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-594563/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein binding to osteoclastogenesis inhibitory factor - useful
                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes an osteoclastogenesis inhibitory factor
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 38; Page 115; 151pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                        calcium metabolism
Sequence 954 BP; 255 A; 239 C; 226 G; 234 T; 0 other;
                                           of the protein, for investigative and diagnostic purposes, and as components of drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW83018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Higashio K, Kinosaki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment and investigation of disorders of bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bone absorption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97JP-0097808.
97JP-0151434.
97JP-0217897.
97JP-0224803.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takahashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    954 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kobayashi F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomoyasu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morinaga T;
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Best Local Similarity

47.3%;

Score 96.4; DB 19 Pred. No. 2.3e-23;

DB 19;

Length 954;

Query Match

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Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV41378 standard; cDNA; 954 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 711 ACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 GCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-1998
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                                                                                                                             This cDNA encodes a human RANKL, a ligand for the RANK (receptor a activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a activator of the tumour necrosis factor (TNF) family. A soluble RANK member of the tumour necrosis factor (TNF) family. A soluble RANK with a soluble rank which binds to expressing membrane-associated RANK with a soluble RANK which binds to expressing membrane-associated RANK with a soluble RANK and can be RANK ligand (RANKL). RANKL polypeptides can activate RANK enhance their used to induce maturation of dendritic cells and enhance their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 CAACATGACTITICAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated ligand for receptor activator of NF-kappa B - used to develop products for augmenting an immune response for inhibiting an inflammatory response and for protection of cells \frac{1}{2} \left( \frac{1}{2} \right) \left(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-377657/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; Pages 59-60; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW69957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Galibert LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0059978.
97US-0813509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0064671.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "human RANKL (ligand for RANK)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maraskovsky E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
New isolated receptor activator of necrosis factor-kappa B - useful
                                                                                       P-PSDB; AAW68293
                                                                                                                   WPI; 1998-377655/32.
                                                                                                                                                                               Anderson DM,
                                                                                                                                                                                                                                   (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                     14-OCT-1997;
23-DEC-1996;
                                                                                                                                                                                                                                                                                             07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9828424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV41372 standard; cDNA; 954 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV41372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease can also be used to identify inhibitors of RANK RANKL Polypeptides an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            711 ACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 GCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           651 TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of TNF-alpha. The products can also be used for detection and drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                         Galibert LJ,
                                                                                                                                                                                                                                                                                97US-0064671.
96US-0059978.
97US-0813509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US23866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "human RANKL (ligand for RANK)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.5%;
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                                                                                                                                                                   Maraskovsky E;

 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.3e-23
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC This cDNA encodes a human RANKL, a ligand for the RANK (receptor CC activator of necrosis factor kappab (NF-kB)) polypeptide. RANK is a CC member of the tumour necrosis factor (TNF) family. Host cells transformed CC nucleic acid can be used to produce recombinant RANK protein. The soluble CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell CC expressing membrane-associated RANK with a soluble RANK which binds to CC used for regulating an immune or inflammatory response. Inhibition of CC Used for regulating an immune or inflammatory response. Inhibition of CC of an inflammatory response that result from triggering of RANK, e.g. in CC inflammatory reactions. They can also be used in adjunct therapy for can also he used to repulsatic cells that express RANK. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
            17-DEC-1998;
                                            07-AUG-2001.
                                                                               US6271349-B1
                                                                                                                                                                 Key
                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                              anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory; ss.
                                                                                                                                                                                                                                Human; receptor activator of nuclear factor kappaB ligand; RANKL; NF; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF; inmune response; inflammatory response; graft-versus-host reaction; toxic shock; sepsis; acute inflammatory reaction; bone resorption;
                                                                                                                                                                                                                                                                                                                   Human receptor activator of NF kappaB ligand (RANKL) cDNA
                                                                                                                                                                                                                                                                                                                                                            15-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           AAD15311 standard; cDNA; 954 BP.
                                                                                                                                                                                                                                                                                                                                                                                                       AAD15311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     711 ACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 GCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     651 TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 TGCCGACATTTGGTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              can also be used for detection and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      591 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Pages 59-60; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for, e.g. developing products for regulating an immune or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory response, treating toxic shock or sepsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 TGAGGCTCATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 47.3%;
Similarity 74.5%;
        98US-0215649
                                                                                               /product= "Human RANK ligand (RANKL) protein"
                                                                                                                                                          Location/Qualifiers
                                                                                                                             /*tag=
                                                                                                                                               .954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 96.4; DB 19; Length 954; Pred. No. 2.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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cc are useful for regulation of immune and intersponse and in screening for inhibitors confidence in the cytoplasmic domain of RANK is used in developing cc of these receptors. The cytoplasmic domain of RANK is used in developing confidence in the cytoplasmic domain of RANK is used in developing confidence in the cytoplasmic domain of RANK is used in developing confidence in the cytoplasmic domain of RANK is used in developing confidence in the cytoplasmic domain of RANK is used in developing confidence in the cytoplasmic domain of RANK is used in developing confidence in the cytoplasmic domain of RANK is used in developing the cytoplasmic domain of RANK with TRAFI, TRAFZ, TRAFZ,
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07-MAR-1997;
14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as adjunct therapy for disease characterized by neoplastic cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dougall WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kappaB (RANK) proteins and their corresponding DNAS. RANK is a member of the tumour necrosis factor (TNF) receptor superfamily and associates with TNF receptor associated factor (TRAF) 2 and 3 which are important in the regulation of immune and inflammatory response. The receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses novel receptor activator of nuclear factor (NF)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7; Column 69-71; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human RANK ligand (RANKL) protein.
                                                                                                                                                                                                                                 531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCCAAGATCTC 590
  177
                                                  651
                                                                                       117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                         591 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
                                                                                                                                                                                      63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                 Match 47.3%;
Local Similarity 74.5%;
                                                                                                                                                                                                                                                                           3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-520313/57
GCTA 180
                                             Galibert L;
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0064671.
96US-0772330.
97US-0813509.
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97US-0077181.
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                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Score 96.4; DB 22; Length 954; pred. No. 2.3e-23;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                 6;
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                                                                                                                                                                                                    Query Match
                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; receptor activator of NF-chi B; RANK; tumour necrosis factor; TNF; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human receptor activator of NF-chi B ligand (huRANKL) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    711 ACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6242213-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-2001
                                                                                                                                                                                                                                                                                  The present invention relates to receptor activator of NF-chi B (RANK) DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to proteins respectively. RANK is a member of the tumour necrosis factor proteins respectively. RANK is a member of the tumour necrosis factor (TRY) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2 region. RANK associates with TNF receptor producing ligands of RANK and TRAF3. The DNA molecules are useful for producing ligands of RANK associates with TNF resembles CD40 in the strategies of RANK. The present sequence is human RANKL (huRANKL) for inhibitors of RANK. The present sequence is human RANKL (huRANKL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi B receptor activator) of the receptor activator of NF-chi B (RANK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anderson DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Column 61-64; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAE04426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-407216/43.
                                                                                                                                                                                                                                      Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                     531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 590
117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                    591 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
                                                                                                                                                                                     Local Similarity
                                                                   63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                    3 TGAGGCTCATAAAACGAGTCTITCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0059978.
97US-0077181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0995659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0064671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Human RANKL protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                            47.38;
74.58;
                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                            Score 96.4; DB 22; Length 954; Pred. No. 2.3e-23;
                                                                                                                                                                                  Indels
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CC The present invention relates to a novel receptor, referred to as RANK CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF (tumour necrosis factor) receptor superfamily. RANK is a Type I CC factors (TRAFs). Triggering of RANK by overexpression or co-expression CC of RANK and membrane bound RANK by overexpression or co-expression CC of the transcription factor NF-kappaB, a ubiquitous transcription factor CC that is most extensively utilised in cells of the immune system.

CC inhibition of Nf-kappaB by RANK antagonists is useful in ameliorating cc negative effects of inflammatory reactions, and the effects of excess CC for the preparation. The RANK DNAs, proteins and their analogues are useful cells for use in gene therapy applications in diagnosing diseases CC may be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct CC osteolysis (FEO) and early onset paget's disease of bone (FEO). The present-sequence is a cDNA encoding full-length human RANKL (hurannel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         멼
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
                                                                                                                                                                                                                                                                 Example 7; Page 75~76; 96pp; English.
                                                                                                                                                                                                                                                                                 New DNA encoding a receptor activator of NF-kappaB polypeptide for the treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAE01993
                                                                                                                                                                                                                                                                                                                                                                          Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                              14-NOV-2000; 2000WO-US31459
                                                                                                                                                                                                                                                                                                                                                                                                (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200136637-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB; NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic; inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial expansile osteolysis; FEO; early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human full-length RANKL (receptor activator of NF-kappaB ligand) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD05904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD05904 standard; cDNA; 954 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       711 ACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 GCTA 180
                                                                                                                                                                                                                                                                                                                                               2001-329222/34.
                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0442029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Human full-length RANKL (receptor activator of NF-kappaB ligand) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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ABK12877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δã
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
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P-PSDB; AAU78286
                 WPI; 2002-304119/34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                               (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT
                                                                                                                        18-AUG-2000; 2000US-226197P.
                                                                                                                                                              20-AUG-2001; 2001WO-US26101
                                                                                                                                                                                                        28-FEB-2002.
                                                                                                                                                                                                                                         W0200216551-A2.
                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; tumour necrosis factor-related activation induced cytokine; TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy; bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis; rheumatoid arthritis; acromegaly; gigantism; exostosis; carilaginea; exostosis bursata; multiple osteocarthritis; contosis; chondrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cartilage growth; skeletal growth; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding human TRANCE protein splice variant 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK12877;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein. The RANKL gene is located in chromosome 13q14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               711 ACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 GCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  651 TGCCAACATTTGGTTTCGACATCATGAAACTTCAGGAGAGCTAGGTACAGAGTATCTTCA 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            591 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
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                                                     Odgren PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                    /note= "Target region for antisense nucleic acid" 95..829
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                                                                                                                                                                                                                                                                                                               /product=
                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
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74.58;
                                                                                                                                                                                                                                                                                                                              o
                                                                                                                                                                                                                                                                                           "Human TRANCE (tumour necrosis factor-related
                                                                                                                                                                                                                                                                             activation induced cytokine) protein,
                                                                                                                                                                                                                                                                         splice variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 96.4; DB 22;
Pred. No. 2.3e-23;
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ABK12876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a new method of treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth. The method of the invention involves administering to the mammal a tumour necrosis factor-related activation induced cytokine (TRANCE)-modulating agent. The method is useful for treating a mammal (TRANCE)-modulating and insufficient or excessive cartilage or skeletal growth, where the disorder comprising insufficient cartilage or skeletal growth is selected from dwarfism, osteopetrosis, cranifesom from the selected from dwarfism osteopetrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resulting from traumatic injury, surgery, osteoarthritis or rheumatoid arthritis, and disorders comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, carilaginea, exostosis bursata and multiple osteocartilaginous exostoses. The method is useful for inhibiting chondrocyte differentiation. The present nucleic acid sequence encodes the human TRANCE protein, splice variant 2, of the invention. TRANCE is a member of the tumour necrosis factor family and acts directly on cartilage-producing cells (chondrocytes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating mammal having disorder characterised by abnormal cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor related activation induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 3; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytokine-modulating agent to mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1945 BP; 623 A; 326 C; 392 G; 601 T; 3 other;
                                                                                                                                                                                               Human; tumour necrosis factor-related activation induced cytokine; TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy; bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis; rheumatoid arthritis; acromegaly; gigantism; exostosis; carilaginea; exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte; exostosis bursata; multiple osteocartilaginous exostosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK12876 standard; cDNA; 2226 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  406 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGGCCAAGATCTC 465
                                                                                                                                                                                                                                                                                                                                      cDNA encoding human TRANCE protein splice variant 1.
                                                                                                                                                                                                                                                                                                                                                                                         18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           466 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             586 ACTA 589
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                                                                   misc_feature
                                                                                                                                                                                cartilage growth; skeletal growth; gene; ss.
                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
       /note= "Tumour necrosis factor (ligand) superfamily, member 11 (TNFSF11), target region for antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 96.4; DB 24;
Pred. No. 3e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the mammal a tumour necrosis factor related activation induced cytokine (TRANCE)-modulating agent. The method is useful for treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth, where the disorder comprising insufficient cartilage or skeletal growth is selected from dwarfism, osteopetrosis, or skeletal growth is selected from dwarfism, osteopetrosis, craniofacial skeletal discrepancies and bone or cartilage damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor related activation induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating mammal having disorder characterised by abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-304119/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choi Y, Odgren PR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resulting from traumatic injury, surgery, osteoarthritis or rheumatoid arthritis, and disorders comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, carilaginea, growth are selected from acromegaly, gigantism, exostoses. The method exostosis bursata and multiple osteocartilaginous exostoses. The method is useful for inhibiting chondrocyte differentiation. The present nucleic acid sequence encodes the human TRANCE protein, splice variant nucleic acid sequence encodes the human TRANCE protein, splice variant 1, of the invention. TRANCE is a member of the tumour necrosis factor 1, of the art after the control of the sequence encodes the human trance of the tumour necrosis factor 1, of the art after the control of the sequence encodes the human trance of the tumour necrosis factor 1, of the art after the control of the sequence encodes the sequence of the tumour necrosis factor 1, of the art after the control of the sequence encodes the sequence of the tumour necrosis factor 1, of the sequence encodes the sequence of the tumour necrosis factor 1, of the sequence encodes the sequence of the sequence of the sequence encodes the sequence of the sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytokine-modulating agent to mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAU78285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             having a disorder comprising insufficient or excessive cartilage or skeletal growth. The method of the invention involves administering to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a new method of treating a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2226 BP; 656 A; 448 C; 505 G; 617 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family and acts directly on cartilage-producing cells (chondrocytes).
AAZ99964 standard; DNA; 2271 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               687 TEGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 746
                                                                                                                                                                                                                                                                                                                                        117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                       747 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 806
                                                                                                                                                            867 ACTA 870
                                                                                                                                                                                                                       177 GCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 47.3%; Score 96.4; DB 24; Length 2226; Local Similarity 74.5%; Pred. No. 3.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                   TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Human TRANCE (tumour necrosis factor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157..1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid. Specifically claimed in claim 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                splice variant 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activation induced cytokine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6;
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Matches
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                                                                                                                                                                                                                                                                                                       protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The of CSF-1 operation describes a method for the in vivo down-regulation of PPGL activity in an animal. The method comprises using at least one OPGL an immune response in the animal. The method and OPGL analogue to induce useful for treating, preventing and ameliorating osteoporosis or other
                                                                                                                                                                                                                                                                 Sequence 2271 BP; 658 A; 462 C; 522 G; 629 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a human osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane
                               117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                              775 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 834
                                                                                                                              715 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 75-77; 110pp; English.
                                                                                     63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTATCAGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
to treat, prevent and ameliorate osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Halkier T, Haaning J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-1998;
02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEBI-) M & E BIOTECH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200015807-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                                                                                  w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding a human osteoprotegerin ligand (OPGL).
                                                                                                                                                                                                                         Match 47.3%;
Local Similarity 74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune response; osteoporosis; bone resorption; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ99964;
TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 894
                                                                                                                                                              TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                137;
                                                                                                                                                                                                                                                                                            or conditions characterised by excessive bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY84417
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0102896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98DK-0001164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "osteoprotegerin ligand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
185..1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                           0;
                                                                                                                                                                                                                Score 96.4; DB 21; Length 2271; Pred. No. 3.2e-23;
                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                      41;
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                6;
                                                                                                                                                                                             Gaps
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Дb δ В QΥ В

Query Match

Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;

47.38;

Score 96.4;

DB 19; Length 2274;

δÃ

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cc encoding Opg binding protein are used to produce recombinant Opg binding components of protein is used in binding assays to determine cc protein. Opg binding protein is used in binding assays to determine cc binding agents (particularly agonists and antagonists, including cc detection of Opg binding protein); to raise Ab (useful in immunoassays for modulate binding of Opg binding protein to osteoclast differentiation cc and activation receptor (ODAR). The nucleic acid molecule encoding Opg Sequences, e.g. screening for related sequences, also to produce cc antisense regulation of Opg binding protein expression. Modulators of Opg binding protein particularly soluble forms of Opg binding protein bone diseases, e.g. osteoporosis, optionally in combination with agents that promote bone growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                           The present sequence encodes human osteoprotegerin (OPG) binding protein. Host cells transfected with vectors containing nucleic acid molecules
                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation
                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 4; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW83195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-594578/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-1998;
16-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human osteoprotegerin binding protein from the pcDNA/huoPGbp1.linsert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypercalcaemia; osteoclast differentiation and activation receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV70285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV70285 standard; DNA; 2274 BP
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97US-0842842.
97US-0880855.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "osteoprotegerin binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Matches

Best Local Similarity Matches 137; Conserv

Conservative

0;

74.58;

Pred. No. 3.2e-23;

Mismatches

41; Indels

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Gaps

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                                                                                                                                                                                                                                                             22-JUN-1999;
20-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immune disorder; anglogenic disorder; gene therapy; cytostatic; neuroprotective; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       715
                                                                                                                                                                                                                            28-JUL-1999;
17-AUG-1999;
31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding human PRO206 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK40274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        775 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 834
                                                                                                                                                                                                                                                                                                                                                                                                                       WO200153486-A1
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22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                        11-FEB-2000; 2000WO-US03565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             895 ACTA 898
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                                                                                                                                                                                                      01-SEP-1999;
15-SEP-1999;
                                                                                                                                                                                                                                                                                                                         11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                   11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, anglogenic and immunologic disorders
                                                                                                                                                                                           30-NOV-1999;
                                                                                                Marsters
                                                P-PSDB; AAU86148.
                                                              WPI; 2002-205567/26.
                                                                                                           Ashkenazi AJ,
                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCCAAGATCTC 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA
                                                                                                                                                          2000WO-US00219
                                                                                    Wood WI;
                                                                                                 Pan J,
                                                                                                            Goddard A,
                                                                                                                                                                                                         99WO-US21090.
                                                                                                                                                                                                                    99US-151689P.
99WO-US20111.
                                                                                                                                                                                                                                          99US-149395P.
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                                                                                                                                                                                                                                                                                                                            99US-133459P
                                                                                                                                                                                                                                                                                                                                                    99WO-US05028.
                                                                                                                                                                       99WO-US28634
                                                                                                                                                                                            99WO-US28313.
                                                                                                 Pitti RM, Roy MA,
                                                                                                              Godowski PJ,
                                                                                                   Gurney AL,
, Smith V,
                                                                                                                   Hillan KJ;
          disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other bladders such as neuronal, glial, astrocytal, hypothalamic, glandular, disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and anglogenic disorders. The polynucleotide sequences are also useful in gene therapy. ABK40254-ABK40288 encode for the human PRO polymentides of the terminal produces and anglogenic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2390 BP; 778 A; 417 C; 506 G; 688 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 50; Fig 41; 302pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1016 ACTA 1019
                                                                                                                                                                                                                                                                                                                                                                         TRANCE; tumour necrosis factor superfamily; signal transduction; TNF; TNF-related activation induced cytokine; immune response; cancer; autoimmune disease; HIV; hypersensitivity; allergen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX80223 standard; cDNA; 1823 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            836 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 895
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human TRANCE encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           956 TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
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                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                               11-DEC-1998;
12-DEC-1997;
                                                                                                                                                                                                                                               W09929865-A2
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                                                                                                                 03-MAR-1998;
                                                                                                                                                                                14-DEC-1998;
                                                                                                                                                                                                                 17-JUN-1999.
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Local Similarity 74.5%;
 P-PSDB; AAY17873
                 WPI; 1999-385609/32.
                                                choi Y,
                                                                              (UYRQ ) UNIV ROCKEFELLER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137;
                                                  Josien R,
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                                                                                                               98US-0989479.
97US-0989479.
98US-0034099.
                                                                                                                                                                                  98WO-US26486
                                                                                                                                                                                                                                                                                                 Location/Qualifiers 1..738
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                                                      Won B;
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Best Local
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       (UYWA-) UNIV WESTERN AUSTRALIA
                                                                 29-SEP-2000; 2000WO-AU01202
                                                                                                                              WO200123549-A1.
                                                                                                  05-APR-2001.
                                                                                                                                                                                                                                                                Rat; osteoclast formation inducer; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                              Rat osteoclast differentiation factor, ODF, coding sequence.
                                                                                                                                                                                                                                                                                                                                  29-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                     AAF86481;
                                                                                                                                                                                                                                                                                                                                                                                           AAF86481 standard; cDNA; 957 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes human TNF-related activation induced cytokines (TRANCE). Human or murine TRANCE polypeptides or their variants, fragments, derivatives or analogues may be used as modulators of immune response in a mammal comprising, antisanse sequences to Agonists and antagonists of TRANCE, can be used to modulate immune cells and increasing or decreasing the life span of mature dendritic are especially useful for treating immune system related conditions such The TRANCE, autoimmune disease or hypersensitivity to an allergen. dendritic cells in vivo or in vitro, especially when used in conjunction with proteins of the tumour necrosis factor (TNF) superfamily (especially with proteins of the tumour necrosis factor (TNF) superfamily (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1823 BP; 569 A; 305 C; 380 G; 569 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      495 ACTA 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
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                                                                                                                                                                                                                                                        Differentiation Factor; bone; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                     99AU-0003147.
                                                                                                                                                         /product= "Rat ODF"
                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.7%;
73.4%;
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Search completed: December Job time : 65.0886 secs
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                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the coding sequence for rat Osteoclast Differentiation Factor (ODF). ODF is thought to be directly involved in Osteoclasts promote dissolution of monocytes/macrophages into osteoclasts. Osteoclasts promote dissolution of the bone matrix and solubilisation of bone salts. The present sequence is useful in gene therapy, and as activity of cells, e.g., cell proliferation, cell differentiation and as vaccines. Anti-rat ODF antibodies are useful in assay methods for
                                                                                                                                                                                                                                                                                                                                                          Sequence 957 BP; 230 A; 260 C; 256 G; 211 T; 0 other;
                                                            659 ACATTTGCTTCAGGCATCATGAAACCTCAGGGAGCGTACCTGCGGACTATCTTCAGCT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid encoding rat osteoclast differentiation factor useful for modulating activity of a cell, e.g., cell proliferation, cell differentiation and cell viability
                                                                                               122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
                                                                                                                                    599 TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 658
                                                                                                                                                                                                          539 CCCATAAAGTCAGTCTGTCCTCTTGGTACCATGATCGAGGCTGGGCCAAGATCTCTAACA 598
                                                                                                                                                                                                                                                                                                                                                                                                  quantifying ODF polypeptides.
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                                                                                                                                                                     68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
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                                                                                                                                                                                                                                                                                                   41.2%; Score 84; DB 22; Length 957; 71.3%; Pred. No. 4.9e-19;
                   8, 2002, 17:26:22

 Mismatches

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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204
1 catgaggctcatamaacgag.....gtamtttgagamtcmttcmc 204
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

20 20 30 30 31 32 33 33 33 33 33 34 34 34 44 44 44 44 44	10 11 13 14 15 16 17 19 19 19 19 21 22 23 24 24 27	Result No. 1 1 2 2 2 5 5 6 6 7 7 8 8 9 9 9
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PAT 13-FEB-2002

ALIGNMENTS

1186 bp Sequence 81 from Patent W00193983.

AX358828.1 GI:18675315

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

SOURCE ORGANISM

KEYWORDS

REFERENCE

AUTHORS

Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watanabe,C.K. and Wood,W.I.

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                               121 GACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Baker.K.P., Desnoyers,L., Gerritsen.M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watanabe,C.K. and Wood,W.I.
                                                                                                                                                                                                                                                                                                                                                                                               Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                 Patent: WO 0208288-A 81 31-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted and transmembrane polypeptides and nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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/db_xref="taxon:9606"
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100.0%; Pred. No. 3.8e-53;
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                                                                                                                                                                                                                                        Sequencing vector: M13: 08
Sequencing vector: M13: 08
Sequencing vector: plasmid; 1008
Chemistry: Dye-primer ET; 08 of reads
Chemistry: Dye-terminator Big Dye; 1008 of reads
Assembly program: phrap; version 0.990319
Consensus quality: 16262 bases at least Q40
Consensus quality: 163189 bases at least Q40
Consensus quality: 164786 bases at least Q20
Insert size: 9479; agarose-fp
Quality coverage: 10.795; sum-of-contigs
Quality coverage: 12.78 in Q20 bases; sgarose-fp
Quality coverage: 10.53 in Q20 bases; sum-of-contigs
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                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: H_NH0254F07
                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site:http://genome.wustl.edu/gsc/index.shtml
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On Apr 30, 2002 this sequence version replaced gi:19339129.
                                                                                                            as soon as it is available and the accession number will
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          Location/Qualifiers
            1112: contig of 1112 bp in length
1212: gap of unknown length
76227: contig of 75015 bp in length
76327: gap of unknown length
165707: contig of 89380 bp in length.
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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The sequence of Homo sapiens BAC clone RP11-95D17
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Direct Submission Senome Sequencing Center, Washington Submitted (20-APR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                             Direct Submission
Submitted (19-APR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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1tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restriction digest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unresolved tandem repeat from base position 181200 to 187300. Size information from restriction digest suggests that the full repeat may not be represented.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The clone sequenced to the left is RP11-521D12. Actual start of this clone is at base position 1 of RP11-95D17; actual end is at base position 190748 of RP11-95D17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are polymorphic base differences between RP11-95D17 and the redundant clone AC062035. Data from AC062035 was used to finish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RP11-95D17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sapiens@watson.wustl.edu
------ Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                 185.
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806. .1114
                                                                                                                                                                                                                                                                                            /rpt_family="L2" 325. .805
                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP11-95D17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
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                                                                                                                /note="similar to
13630. .14128
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13614. ,14110
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                            EST BF770793 (NID:g12118693)"
                                                        EST BF770127 (NID:g12118027)"
                                                                                    EST BF770134 (NID:g12118034)"
                                                                                                                                           EST BF770132 (NID:g12118032)"
                                                                                                                EST BF770135 (NID:g12118035)"
                                                                                                                                                      FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 174428 CATGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTC 174369
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                                                                                                                                                                                                                                                     AUTHORS
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                                                                CDS
                                                                                            gene
                                                                                                                                    source
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                                                                                                                                            Direct Submission Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                 Determination of human RANKL isoforms
                                                                                                                                                                                                                                                   Ikeda,T.
                                                                                                                                                                                                                                                                                                  Ikeda, T., Kuroyama, H. and Hirokawa, K.
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens hRANKL 3 mRNA for receptor activator of nuclear factor ABD64268
                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens cDNA to mRNA.
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                                                                                                                                                                                                                                                             (bases 1 to 818)
/product="receptor activator of nuclear factor kappa
                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                           and Kuroyama, H.
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                                                                                                                                           Location/Qualifiers
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13729. .14126
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              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABUUJ142/
HOMO Sapiens mRNA for hRANKL 2, complete cds.
AB061227
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-MAY-2001) Tohru Ikeda, Graduate School, Tokyo Medical and Dental University, Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
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                                                                                                                                   /protein_id="BAB71768.1"
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SWLDLAKRSKLEAQFFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLI
VNQDGFYYLYANICFRHHETSGDLATEYLQLMYYVTKTSIKIPSSHTLMKGGSTKYWS
                                                                                                             GNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kuroyama, H. and Hirokawa, K.
                                                                                                                                                                                                                                                                               /product="hRANKL 2"
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                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
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pred. No. 8.7e-21;
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Pred. No. 8.7e-21;
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al Similarity
137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (26-JAN-2000) Masazumi Nagai, Iwate Medical University School of Dentistry, Department of Biochemistry; 19-1 Uchimaru, Morioka, Iwate 020-8505, Japan (E-mail:mnagal@iwate-med.ac.jp, Tel:+81-19-651-5111(ex.4436), Fax:+81-19-654-4147)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EVSNPSLLDPDDDATYFGAFKVRDID"
184 c 200 g 260 t 3 others
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                                                                                                                                              RIKOAFOGAYOKELOHIVGSOHIRAEKAMYDGSWLDLAKRSKLEAOPFAHLTINATDI
PSGSHKVSLSSWYHDRGWAKISNWIFSNGKLIVNODGFYYLYANICFRHHEITSGDLAT
                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
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/protein_id="BAA90488.1"
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                                                                                                                                                                                                                                                                         /gene="sOdf/trance"
                                                                                                                                                                                                                                                                                                                                                /cell_type="epithelial-like squamous cell cacinoma"
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                                                                                                                                                                                                                                                                                                                                                                                     /cell_line="SCC-4"
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                                                                                                                                                                                                                                                                                                              /gene="sOdf/trance"
                     47.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        137;
         1 (bases 1 to 954)
Dougall,W.C. and Galibert,L.
Receptor activator of NF-.kappa.B
Patent: US 6271349-A 12 07-AUG-2001,
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                                                                 Unclassified.
                                                                                                                              Sequence 12 from patent US AR164148
                                                                                            Unknown.
                                                                                                                 AR164148.1 GI:16235114
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Isolated DNA molecules encoding RANK-L
Patent: US 6242213-A 12 05-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unclassified.
1 (bases 1 to 954)
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239 c 227 g
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117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                           591 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
                                                                                                                                531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 590
                                                                                  63 CAACATGACCTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                          3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 47.3%;
Local Similarity 74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson,D.M. and Hughes,A.E.
Receptor activator of nf-kappa b
Patent: WO 0136637-A 12 25-MAY-2001;
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TLESQDTKLIPDSCRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKL
EAQPFAHLTINATD1PGSGHKYSLSSWYHDRGWAKISNWTFSWKKLIVWQDGFYYLYA
NIGFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSIN
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74.58;
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                                                                                                        AB064270 972 bp mRNA linear PRI 26-DEC-
Homo sapiens hranKL 2-2 mRNA for receptor activator of nuclear
factor kappa B ligand 2-2, complete cds.
Homo sapiens cDNA to mRNA
                                                            AB064270.1 GI:18143620
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/translation="MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAA
SRSMFVALLGLGIGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRHEMADFQDT
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EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNWTESNGKLIVNGOGFYYLYA
NICFRHHETSGDLATEKLQLMWYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSIN
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239 c 227 g 233 t
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/db_xref="GI:21698736"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AB064269
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                    AB064269.1 GI:18143618
                                                                                 Ikeda, T., Kuroyama, H. and Hirokawa, K.
                                        Determination of human RANKL isoforms
                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                  Homo sapiens cDNA to mRNA.
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/protein_id="BaB79695.1"
/db_xref="GI:18143621"
/translation="MYVALLGIGEIGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRIL
/translation="MYVALLGIGEIGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRIL"
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                                         9367155
                                                                growth and dendritic-cell functio
                                                                         A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function
                                                                                                                        Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C., Tometsko,M.E., Roux,E.R., Teepe,M.C., DuBose,R.F., Cosman,D.
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2201)
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                     (bases 1 to 2201)
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da,T. and Kuroyama,H.
                                                                                                                                                                                                                                                                                                    mRNA, complete cds.
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SRSMFVALLGLGLGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDT
TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKANVDGSWLDLAKRSKL
EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYA
NICFRHHETSGDLATEVLQLMYYVTKTSIKIPSSHTLMKGGSTKYMSGNSEFHFYSIN
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257 c 265 g 237 t
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117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTATCCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity les 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 838
                                                 lacey,D.L., Timms.E., Tan,H.-L., Kelley,M.J., Dunstan,C.R., Burgess,T., Elliott.R., Colombero,A., Elliott.G., Scully,S., Hsu,H., Sullivan,J., Hawkins,N., Davy,E., Capparelli,C., Eli,A., Olan,Y.-X., Kaufman,S., Sarosi,I., Shalhoub,V., Senaldi,G., Guo,J., Delaney,J. and Boyle,W.J.
Cell 93 (2), 165-176 (1998)
       Osteopprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                          AF053712.1 GI:3057145
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens osteoprotegerin ligand mRNA, complete cds
                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson,D.M., Billingsley,W., Dougall,W., Maraskovsky,E., Cosman,D., DuBose,R. and Galibert,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MRRASRDYTKYLRGSEEMGGGGGGAPHEGPLHAPPPPAAPHQPPAA
SRSMFVALLGLGLGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRHENADFQDT
TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIYGSGHIRAFRAWDGGSWLDLAKRSKL
EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISHTFSNGKLIVNQDGFYYLYA
NICFRHHETSGDLATEYLQLMYYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSIN
VGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="RANKL"
129. .1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAB86811.1"
/db_xref="GI:2612922"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="RANKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="RANKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="receptor activator of nuclear factor kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="13q14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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74.5%;
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Pred. No. 8.8e-21;
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Search completed: December Job time: 553.856 secs
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Best Local Similarity
Matches 137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 GCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                    895 ACTA 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      775 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
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Boyle,W.J.
Direct Submission
Direct Submission
Submitted (16-MAR-1998) Department of Cell Biology, Amgen, In
Submitted Center Drive, Thousand Oaks, California 91320, USA
One Amgen Center Drive, Thousand Oaks, California 91320, USA
1 27771
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/Codon_start=1
/Codon_start=1
/product "osteoprotegerin ligand"
/product "osteoprotegerin ligand"
/protein_id="AaC39731.1"
/protein_id="AaC39731.1"
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/db_xref="taxon:9606"
185. .1138
                                                                                                                              8, 2002, 18:33:58
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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Perfect score:
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16154066 segs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 atggcaatcctgacgctcag.....gtaatttgagaatcattcac
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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37	37	38.6	71	84.8	95.8	Score
14.2	14.2	14.8	27.2	32.5	36.7	Query Match
277	276	198	362	612	659	Query Match Length DB
12	12	12	10	17	17	DB
BG184205	BG203357	BG197160	AV653073	вн267783	AG107545	DB ID
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17	17	17	13	17	17	17	12	17	10	9	17	12	17	14	10	17	17	17	13	10	10	17	17	9	12	17	14	17	17	17	10	10	14	12	17	17	12
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ALIGNMENTS

RESULT 1 AG107545 REFERENCE SOURCE VERSION ACCESSION DEFINITION COMMENT REFERENCE KEYWORDS LOCUS ORGANISM TITLE AUTHORS TITLE AUTHORS JOURNAL JOURNAL 2 (bases 1 to 659)
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Totoki,Y., Watanabe,H. and Sakaki,Y. Pan troglodytes Unpublished BAC end sequences of Library PTB GSS 03-NOV-2001

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                                                                              Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources
                                 (http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 186 row: C column: 1
                                                                                                                                                                                                                             Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143;
                                                                                                                                                                          Email: szhao@tigr.org
                                                                                                                                                                                             Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Other_GSSs: CH230-186C1.TJ
                                                                                                                                                                                                                                                                                                                                             Rat BAC End Sequences from Library CHORI-230 EcoRI segment
                                                                                                                                                                                                                                                                                                                                                                  Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., of Jong,P. and Fraser,C.M.
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CH230-186C1.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     603 TCTCTCTAGGTTCCCATAAAGTCAGTCTGTCCTCTTGGTACCATGATCGAGGCTGGGCCA 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 TATCCCATGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCTTCAGCT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTGTACGCCAACATTTGCTTCAGGCATCATGAAACCTCAGGGAGCGTACCTGCGGACT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132;
                                                                                                                                                                                         Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, p. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                    Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma by comparing gene expression profiles of hepatocellular carcinoma proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                     Email: hanzg@chgc.sh.cn
This clone is available at CHGC in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 362)
Xu, Z., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV653073 GLC Homo sapiens cDNA clone GLCDHB01 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV653073.1 GI:9874087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV653073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                   /organism="Homo sapiens'
/db_xref="taxon:9606"
/tissue_type="corresponding non cancerous liver tissue"
                               /clone_lib="GLC"
                                                     /clone="GLCDHB01"
                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="fector: pTARBAC2.1; Site_1: ECORI; Site_2: ECORI; CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by Pieter de Jong" 145 c 133 g 166 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="CHORI-230 Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="Brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="CH230-186C1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                    . 362
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Pred. No. 1.6e-17;
0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 bp
                                                                                                                                                        Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE
                                                                                           Best Local Similarity Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCCATCTG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 ACATGACTTTCAGC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 GCT--CATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                              4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTAATACCATCAATATCCCCATGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACATGACTTTTAGC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 198)

1 (bases 1 to 198)

1 (cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith, Lerner,L., Mays,R., McMays,R., McMays,R., Mays,R., McMays,R., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG197160 198 bp mRNA linear EST 21-APR-2
RST16397 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG197160
ESI
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3201 Carnegie Ave, Cleveland, OH 44115, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 a
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                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="Adult"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                         /note="See" (Treation of Genome-wide Protein Expression /note="See" (Treation of Genome-wide Protein Expression', Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the nearly periodicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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75.4%;
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Pred. No. 5.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 g
                                                                                                           0,
                                                                                                                                      Score 38.6; DB 12; Length 198;
Pred. No. 0.038;
                =
                                                                                                           Mismatches
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             2 others
                                                                                                                      Indels
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                                                                                                                                                                                                                                        Db
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                                      SOURCE
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                                                                            VERSION
                                                                                                 DEFINITION ACCESSION
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                                                           KEYWORDS
                                                                                                                                      Cocus
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATGTG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                              64 G 64
                                                                                                                                                                                                                                          7 G 7
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1 (bases 1 to 276)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Gain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.
Cain, S., Leventhal, C., McElligott, K., Boozer, S., Mays, R., Smith
Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith
Lerner, L., Costanzo, D., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher
, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher
, J., Danzig, J. and Ducar, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG203357
2/6 DP MIKNE THUGE BG203357
RST22738 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
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BG203357.1 GI:13725044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3201 Carnegie Ave, Cleveland, OH 44115, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: scain@athersys.com
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                             BG184205.1 GI:13705892
EST.
                                                                                                 BG184205 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
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216 361 9596
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/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
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75.4%;
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pred. No. 0.15;
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Local Similarity 75.48;
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                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 299)

Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher Creation of genome-wide protein expression libraries using random Nat. Biotechnol. 19 (5), 440-445 (2001)
                       Tel: 216 431 9900
Fax: 216 361 9596
                                        Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
                                                                                                 Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3201 Carnegie Ave, Cleveland, OH 44115, USA
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Fax: 216 361 9596
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scain@athersys.com
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/db_xref="taxon:9606"
/Clome_lib="Athersys RAGE Library"
/cell_line="HT1080"
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Pred. No. 0.15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G 30
                                                                                                                                                                                               library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end Plate: 210 row: N column: 16 seq primer: SP6 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
Clones are derived from the mouse BAC_library RPCI-24. For BAC
                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Other_GSSs: RPCI-24-210N16.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
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/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                                                          /sex="Male"
                                                                            /clone_lib="RPCI-24"
                                                                                          /db_xref="taxon:10090"
/clone="RPCI-24-210N16"
                                                                                                                                   /strain="C57BL/6J"
                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                         Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
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75.4%;
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Pred. No. 0.16;
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BH671765/c
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168 CCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCT 221
                                                                                                                                                                                  48 ATCAATATCCCATGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTG 107
                                                                                                                                                                                                                                           Local Similarity
                                                                        GGAAATCTTCTAATACATAATAATGAGAAGAATCCATCTACTAGGAAAAGGAAAGGGTTT 579
                                                                                                            GCCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTA 167
                                                                                                                                               ATRAGGATTACAAGATGAAGATAAATGGAAAGTATCCAAAACCTAAACTCACTAAGATTA 639
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BH671765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOMKY36TR BO_2_3_KB Brassica oleracea genomic clone BOMKY36, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH671765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica oleracea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cdtown@tigr.org
DNA is from a doubled haploid provided by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: sheared ends.
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                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                      /Clone_lib="BO_2_3.KB"
/Clone_TVector: pHOS1; Site_1: BstXI; 2-3 kb sheared fonce="Vector: pHOS1; Site_1: BstXI linkers"
genomic DNA inserted into pHOS1 using BstXI linkers"
1.44 c 162 g 192 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Brassica oleracea"
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                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:3712"
/clone="BOMKY36"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="TO1000DH3"
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57.7%;
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Pred. No. 0.
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    161 ACAGCTT 167
                                                                                        155 AAGGCAT 161
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., decliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
Brunstein,A., decliveira,P.S., Bucher,P., Jongeneel,C.V., and
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
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Ludwig Institute for Cancer Research
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Seq primer: puc 18 forward
High quality sequence stop: 462.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue mRNA and cDNA amplification were performed under low stringency conditions. To 97 c 115 g 95 t
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                                                       81 TTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGG 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further i
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanne, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schur, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           /note-Tvector: pBluescript II SK+; Site_1: EcoRI; Site_2: NhOI; The cDNA library was constructed from mRNA isolated from degenerating cotyledons of 9-10 day old etiolated seedlings for the cultivar Williams. Complementary DNA was poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were transformed into the EcoRI-XhoI restriction site were transformed into DH10B host cells (GibcoBRL). This
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                                                                                                                                                                                             141 AAAACTAAGAGTCAAAGGCATTTATTACCGG 171
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BE346444 475 bp mRNA linear EST 04-DEC-2001 sp25f04.yl Gm-c1042 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Gijzen M
Agriculture and Agri-Food Canada
1391 Sandford Street Tondon on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene expression in developing soybean seed coats Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: gijzenm@em.agr.ca
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//Ab_host="E_coli host strain XLOLR"
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519 457 1470
519 457 3997
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                                                                                                                                                              156 CCTAGTTCTTAGCTCCTCAATAAGTTCATCAAGAACGCAAAATGCCAATGGCATGGCACT 97
                                        141 AAAACTAAGA 150
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                                                                                Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanne,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
AGAACACAGA 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 475.
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Washington University School of Medicine
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314 286 1810
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                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         from 2 week old seedlings with the cotyledons removed at the time of harvest. The seedlings for the cultivar Raiden were grown in a growth chamber using germination paper. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DHIOB host cells (Gibco BNL). This were transformed into DHIOB host cells (Gibco BNL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="GENOME SYSTEMS CLONE ID: Gm-c1042-1592"
/clone_lib="Gm-c1042"
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                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                            Score 34; I
Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                          102 g
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AF046628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 TNAAAATATTA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 TGGAAACATGA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF046628 Mus musculus 129Sv/Ev Mus musculus genomic clone OST1450,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF046628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 392 (6676), 608-611 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disruption and sequence identification of 2,000 genes in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 563)
Zambrowicz, B.P., Fr
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: materials@lexgen.com
OmniBank Sequence Tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4000 Research Forest Drive, The Woodlands, TX 77381, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OmniBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Zambrowicz BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Person, C. and Sands, A.T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lexicon Genetics Incorporated
                                                                                                                                                                                                                                                                                                                                                                    AG132233
AG132233.1 GI:16661911
GSS.
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Similarity 64.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  AG132233 631 bp DNA linear GSS 04-NOV-200 Pan troglodytes DNA, clone: PTB-144II7.F, genomic survey sequence.
submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (SSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                            Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                      Pan troglodytes
                                                                  Direct Submission
                                                                                                         Fujiyama, A.,
                                                                                                                                                   Unpublished
                                                                                                                                                                          BAC end sequences of Library PTB
                                                                                       Totoki,Y., Watanabe,H. and Sakaki,Y
                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150
                                                                                                                                                                                                                                                                                                                        troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male Library clone:PTB-144117.F.
                                                                                                                                   (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST1450"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="embryonic stem cell" 118 c 119 g 137 t
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                                                                                                                              1 to 631)
                                                                                                                                                                                                                                                                                 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                            Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Friedrich, G.A., Buxton, E.C., Lilleberg, S.L.,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Search completed: December 8, 2002, 19:27:07 Job time: 589.736 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                         Query Match 13.0%; Score 34; DB 17; Length 631; Best Local Similarity 57.5%; Pred. No. 2.3; Matches 61; Conservative 0; Mismatches 45; Indels
                                                                      173 TCAAACTTCGTTGATAGAAGGAAATGTAAGTTTAGGGAGAGTGAAA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                           99 CCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY
                                                                                                                                                                                                                                                                                                                                  181 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing: -21M13
                                                                                                                                                                                                                                                                                                                /cell_type="lymphoblast"
/clone_lib="pTB Chimpanzee Male BAC Library"
/clone_lib="pTB Chimpanzee Male BAC Library"
/clone_lib="pTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                       /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-144I17.F"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .631
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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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            N_Geneseq_101002:*
1: /SIDS2/gcgdata/gc2: /SIDS2/gcgdata/gc3: /SIDS2/gcgdata/gc3: /SIDS2/gcgdata/gc3: /SIDS2/gcgdata/gc3: /SIDS2/gcgdata/gc3: /SIDS2/gcgdata/gc3: /SIDS2/gcgdata/gc3: /SIDS2/gcgdata/gc3: /SIDS2/gcgdata/lc2: /SIDS2/gcgdata/lc2: /SIDS2/gcgdata/lc2: /SIDS2/gcgdata/lc3: /SID
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261
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1: \SIDS2\gcgdata\geneseq\geneseqn-emb1\NA1980.DAT:*
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Listing first 45 summaries
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

9	æ	7	σ	σ	4	ω	N	<u>, , , , , , , , , , , , , , , , , , , </u>	Result No.
121.2	121.2	121.2	121.2	121.2	121.2	121.2	121.2	251	Score
46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4		Query Match Length DB
1945	954	954	954	954	954	954	741	1186	Length
24	22	22	22	19	19	19	19	24	
ABK12877	AAD05904	AAD08715	AAD15311	AAV41372	AAV41378	AAV69887	AAV69899	ABK33576	ID
cDNA encoding huma	Human full-length	Human receptor act	Human receptor act	NF-kB receptor act	NF-kB receptor act	Nucleic acid encod	Nucleic acid encod	cDNA encoding huma	Description

	10 11 11 11 11 11 11 11 11 11 11 11 11 1
	1121121 1121121 1121121 1121121 112112 112112
	11111222222223333333333333333333333333
	2226 22271 22271 182390 182390 7359 951 951 951 1630 1630 1630 1630 1630 1630 22291 22295 5199 5199 5199 5199 5199 51
	224 224 227 227 227 227 227 227 227 227
ALIGNMENTS	ABK12876 AAV799964 AAV70285 ABK40274 ABK40274 AAV80823 AAF86481 AAV69898 AAV69990 AAA39156 AAL299965 AAV41377 AAV41377 AAV41377 AAV41377 AAV41489 AAV69898 AAV99966 AASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
	CDNA encoding huma DNA encoding a hum Human osteoprotage cDNA encoding huma Human TRANCE encod Rat osteoclast dif Nucleic acid encod Nucleotide sequenc Nurine receptor act Murine receptor ac Murine receptor ac Murine RANKL (rece Nucleotide sequenc Murine TRANCE enco CDNA encoding mous Human osteoprotage DNA encoding a mur Mouse OBM nucleoti DNA encoding a syn DNA encoding osteo DNA sequence SEQ CDNA sequence SEQ CER encoding CDNA.

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                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to one hundred and twenty two nucleic acids CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides CC encode human secreted proteins. The PRO nucleic acids, polypeptides, CC agonists and antagonists are useful for treating a PRO related disorder. CC The PRO polypeptides are useful for diagnosing tumours, especially lung CC cancer, colon cancer, breast tumour prostate tumour, rectal tumour or CC liver tumour. The PRO polypeptides are useful for stimulating the CC the proliferation of, or gene expression, in pericyte cells, for stimulating the relasse of tumour necrosis factor-alpha from human blood, CC for stimulating or inhibiting the proliferation of normal human deermal CC fibroblast cells. The PRO polypeptide may also be used as molecular CC applications in molecular biology, including use as hybridisation probes, CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human CC PRO protein coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1186 BP; 314 A; 285 C; 299 G; 288 T; 0 other;
                                                                                                                                                                                                                                                             447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2000;
23-AUG-2000;
24-AUG-2000;
15-SEP-2000;
10-NOV-2000;
 687
                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Figure 81; 359pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumour or liver tumour -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-172001/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2001;
10-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-2000;
01-DEC-2000;
                                                                                                                                                                                                                    61 GAGGCTCATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                     1 ATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTAATAACATCATCAATAATCCCAT 60
                                                                       ATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTATGG 240
                                                                                                                                       AACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGAC 180
                                                                                                                                                                                     TGTAATTTGAG 251
TGTAATTTGAG 697
                                                        ATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTATGG
                                                                                                                       AACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGAC
                                                                                                                                                                                                                                                    ATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCAT 506
                                                                                                                                                                                                                                                                                                                                           Similarity
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C, Gurney AL,
                                                                                                                                                                                                                                                                                                                              Conservative
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2000WO-US23522
2000WO-US23328
2000US-000000P
2000WO-US30673
2000WO-US30676
2000WO-US32676
2000WO-US32676
2000WO-US32676
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2001US-0854280
                                                                                                                                                                                                                                                                                                                                          96.2%; Score 251; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerritsen ME, Goddard A, Godowski I
Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                          3e-74;
                                                                                                                                                                                                                                                                                                                                                  DB 24; Length 1186;
                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                         Indels
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RESULT

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64 GCT--CATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGGAAACGTCTCCA 121

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                                                                Matches
                                                                                            Query Match
                                                                               Best Local
                                                                                                                                                     The present sequence encodes an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone of the protein, for investigative and diagnostic purposes, and as
                                                                                                                 Sequence 741 BP; 230 A; 153 C; 158 G; 200 T; 0 other;
                                                                                                                                                   components of drugs.
                                                                                                                                                                                                                                                                                                                                                                      Example 28; Pages 121-122; 151pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                      calcium metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goto M, Higashio K, Kinosaki M, Kobayas
Nakagawa N, Shima N, Takahashi K, Tomoy
Washida N, Yamaguchi K, Yano K, Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                              Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-594563/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUN-1997;
12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM; osteoclast; bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L5-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid
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                           4 GCAATCCTGACGCTTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG
                                                                181;
                                                                            Similarity
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding a human OCIF-binding molecule (OBM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97JP-0332241.
97JP-0097808.
97JP-0151434.
97JP-0217897.
97JP-0224803.
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                                                                         46.48;
74.88;
                                                           0;
                                                                     Score 121.2; DB 19; Length 741; Pred. No. 1.4e-30;
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kobayashi F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tomoyasu A,
                                                          53;
                                                           Indels
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Tsuda E;
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RESULT 3
AAV69887
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09-JUN-1997;
12-AUG-1997;
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                                                                The present sequence encodes an osteoclastogenesis inhibitory factor (OCIF) binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins absorption factor by separation and solubilisation of membrane proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9846644-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoclast; bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV69887 standard; cDNA to mRNA; 954 BP
                                                                                                                                                                                                            Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-1997;
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                                                                                                                                                                   Claim 38; Page 115; 151pp; Japanese
                                                                                                                                                                                                                                                      P-PSDB; AAW83018.
                                                                                                                                                                                                                                                                    WPI;
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                                                                                                                                                                                e.g. Lieu
cium metabolism
           affinity chromatography using OCIF. It exists in a full-sequence and a solubilised form (sOBM) which is a shorter chain. OBM may be for screening potential inhibitors and modifiers of its biological vity, and screening for receptors to OBM which mediate its function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGAGCCTAGCTACAGAGTATCTTCAAC 499
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                                                                                                                                                                                                                                                                                    N, Yamaguchi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding a human OCIF-binding molecule
                                                                                                                                                                                                                                                                                                                                                                             97JP-0332241.
97JP-0097808.
97JP-0151434.
97JP-0217897.
97JP-0224803.
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N, Takahashi K,
hi K, Yano K, Y
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be used
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                                                                                                                                                                                                                                                                                               Yasuda
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asuda H;
 the treatment of disorders
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RESULT 4
AAV41378
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                                                                                                                                                14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      function and calcium metabolism. The antibodies can be used of the protein, for investigative and diagnostic purposes, a components of drugs.
         New isolated ligand for receptor activator of NF-kappa develop products for augmenting an immune response for inflammatory response and for protection of cells
                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                              RANK; necrosis factor-kappa B; NF-kB; receptor activator; hu immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 954 BP; 255 A; 239
                                                                        WPI; 1998-377657/32.
                                                                                                 Anderson DM,
                                                                                                                                                                                                   22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                 NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV41378 standard; cDNA; 954
                                                             P-PSDB;
                                                                                                                                                                                                                           02-JUL-1998.
                                                                                                                                                                                                                                                  WO9828426-A2
                                                                                                                       (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           713
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                                                             AAW69957
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                                                                                                 Galibert
                                                                                                                                                97US-0064671.
96US-0059978.
97US-0813509.
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                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                           /product= "human RANKL (ligand for RANK)"
                                                                                                                                                                                                                                                                                          /*tag=
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74.88;
                                                                                                 LJ,
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                                                                                                 Maraskovsky
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Pred. hes 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 121.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 T; 0 other;
                                                                                                 E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19;
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                      inhibiting
                                    B - used to
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The may be used for inhibiting activation of NF-KB, by contacting a cell cexpressing membrane-associated RANK with a soluble RANK which binds to CRANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their callostimulatory capacity, thereby augmenting an immune response. The coluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-KB by RANK antagonists composite that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory caractions. They can also be used in adjunct therapy for disease contaracterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK expressing cells from the negative effects of chemotherapy or the presence of high levels of TNF-alpha. The products can also be used for detection and drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                                                          Key
                WO9828424-A2
                                                                                                                                                  Homo
                                                                                                                                                                                                      RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis;
                                                                                                                                                                                                                                                            NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
                                                                                                                                                                                                                                                                                                      08-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 AAV41372 standard; cDNA; 954 BP
                                                                                                                                                                                                                                                                                                                                              AAV41372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This cDNA encodes a human RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is member of the tumour necrosis factor (TNF) family. A soluble RANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 954 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; Pages 59-60; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         653 CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC
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Local Similarity 74.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC
                                                                                                                                                  sapiens
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                                                                                                                                                                                      response; in RANK ligand;
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                                              /product= "human RANKL (ligand for RANK)"
                                                                      /*tag=
                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                      tumour necrosis factor;
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23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANK ligand (RANKL). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of MF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. The products
                                                                                                         AAD15311 standard; cDNA; 954 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This cDNA encodes a human RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. Host cells transformed or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to
                               15-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            can also be used for detection and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated receptor activator of necrosis factor-kappa B for, e.g. developing products for regulating an immune or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory response, treating toxic shock or sepsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 46.4%;
Local Similarity 74.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTAATACCATCATCAATATCCCATGAG 63
                                                                                                                                                                                                                                          TA 237
                                                                                                                                                                                                                                                                                                                                                        ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG
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96US-0059978.
97US-0813509.
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Pred. No. 1.5e-30;
0; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 19; Length 954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53; Indels
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Human receptor activator of NF kappaB ligand (RANKL) cDNA

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The patent discloses novel receptor activator of nuclear factor (NF)-CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member CC of the tumour necrosis factor (TNF) receptor superfamily and associates CC with TNF receptor associated factor (TRAF) 2 and 3 which are important CC in the regulation of immune and inflammatory response. The receptors CC are useful for regulating immune response and in screening for inhibitors of signal transduction, e.g. for screening the CC molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, CC TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists are useful in ameliorating the negative effects of an inflammatory CC response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, acute inflammatory CC reactions and the effects of bone resorption. RANK from apoptosis. CC soluble forms of the receptor are used in vivo or in vitro based CC screening tests for agonists or antagonists of RANK acts as an anticular through the form and rescue the cells that express RANK from apoptosis. CC adjunct therapy for disease characterised by neoplastic cells that CC express RANK. Compounds that interfere with RANK promostic cells that CC express RANK. Compounds that interfere with RANK/TRAF6 interactions are useful for modulating osteoclast function and activities. They care useful for the expressants or anti-inflammatory agents. The RANK DNAs are useful for the expressants or anti-inflammatory agents. The RANK DNAs are useful for the expressants or anti-inflammatory agents. The RANK DNAs are useful for the expressants or anti-inflammatory agents. The RANK DNAs are useful for the expressants or anti-inflammatory agents. The RANK DNAs are useful for the expression of recombinant proteins, as probes for analysis of the presence or distribution of RANK transcripts, while the proteins conditions are useful for the detection of soluble RANK, or monitor RANK. Pagated activity. The present sequence is a cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as adjunct therapy for disease characterized by neoplastic cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-apoptotic
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07-MAR-1997;
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07-MAR-1997;
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human RANK ligand (RANKL)
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97US-0813509.
97US-0996139.
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97US-0064671
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/product= "Human RANK ligand (RANKL) protein"
protein.
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1996;
07-MAR-1997;
14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 954 BP; 255 A; 239
The present invention relates to receptor activator of NF-chi B DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL)
                                                                                      Claim 2; Column 61-64; 43pp; English.
                                                                                                                                                 New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi receptor activator) of the receptor activator of NF-chi B (RANK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; receptor activator of NF-chi B; RANK; tumour necrosis factor; TNF; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human receptor activator of NF-chi B ligand (huRANKL) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6242213-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473
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                                                                                                                                                                                                                                                                       2001-407216/43
DB; AAE04426.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΤA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTCCA 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCT--CATAAAACGAGTCTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC
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97US-0077181.
97US-0064671.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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74.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Human RANKL protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB; MF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic; inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial expansile osteolysis; FEO; early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2 and TRAF3. The DNA molecules are useful for producing ligands of RANK. The ligands are useful for regulating immune response and in screening for inhibitors of RANK. The present sequence is human RANKL (huRANKL)
Anderson DM,
                                                                          (IMMV ) IMMUNEX CORP
                                                                                                                                         17-NOV-1999;
                                                                                                                                                                                                            14-NOV-2000; 2000WO-US31459.
                                                                                                                                                                                                                                                                                                                                                  WO200136637-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human full-length RANKL (receptor activator of NF-kappaB ligand) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD05904 standard; cDNA; 954 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 TA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473 GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              713 TA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              533 GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCCAAGATCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           593 ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACATGACTITCAGCAACGGAAAACTAAGAGTCA-----AAGGCATITATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC
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   Hughes AE
                                                                                                                                         99US-0442029.
                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Human full-length RANKL (receptor activator
of NF-kappaB ligand) protein"
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Pred. No. 1.
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es 53; Indels
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RESULT 9
ABK12877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibition of Nf-kappaB by RANK antagonists is useful in ameliorating negative effects of inflammatory reactions, and the effects of excess bone resorption. The RANK DNAs, proteins and their analogues are useful for the preparation of pharmaceutical compositions, for infecting target cells for use in gene therapy applications in diagnosing diseases associated with RANK, and as targets for use in screening assays. They may be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct gene-activating mutations, associated with e.g. familial expansile osteolysis (FEO) and early onset paget's disease of bone (EP). The present sequence is a cDNA encoding full-length human RANKL (hurankil) protein. The RANKL gene is located in chromosome 13q14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a novel receptor, referred to as RANK (receptor activator of NF (nuclear factor)-kappaB), a member of TNF (tumour necrosis factor) receptor superfamily. RANK is Type I transmembrane protein that interacts with TNF receptor-associated factors (TRAFS). Triggering of RANK by overexpression or co-expression of RANK and membrane bound RANK ligand (RANKL) results in upregulation of the transcription factor NF-kappaB, a ubiquitous transcription factor that is most extensively utilised in cells of the immune system.
                  TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy; bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis; rheumatoid arthritis; acomegaly; gigantism; exostosis; carilaginea; exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;
                                                                                                           Human; tumour necrosis factor-related activation induced cytokine;
                                                                                                                                                       cDNA encoding human TRANCE protein splice variant 2.
                                                                                                                                                                                                     18-JUN-2002
                                                                                                                                                                                                                                                    ABK12877;
                                                                                                                                                                                                                                                                                              ABK12877 standard; cDNA; 1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; Page 75-76; 96pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA encoding a receptor activator of NF-kappaB polypeptide for the treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 46.4%;
Local Similarity 74.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCCAAGATCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCT--CATAAAACGAGTCTTTCTTCGTAGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG
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skeletal growth;
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Pred. No. 1.5e-30;
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                                                                                                                                                                                                                                                                                                                                          (TRANCE)-modulating agent. The method is useful for treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth, where the disorder comprising insufficient cartilage or skeletal growth is selected from dwarfism, osteopetrosis, craniofacial-skeletal discrepancies and bone or cartilage damage resulting from traumatic injury, surgery, osteoarthritis or rheumatoid arthritis, and disorders comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, carilaginea, exostosis bursata and multiple osteoarthlaginous exostoses. The method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a new method of treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth. The method of the invention involves administering to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating mammal having disorder characterised by abnormal cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor-related activation induced cytokine-modulating agent to mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200216551-A2
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                                                                                                                                                                                                                                                                       is useful for inhibiting chondrocyte differentiation. The present nucleic acid sequence encodes the human TRANCE protein, splice variant 2, of the invention. TRANCE is a member of the tumour necrosis factor family and acts directly on cartilage-producing cells (chondrocytes).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2001; 2001WO-US26101
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                                                                                                                                                                                                                                          Sequence 1945 BP; 623 A; 326 C; 392 G; 601 T; 3 other;
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                                                                                                                                       4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
                                                                                                                                                                                        ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mammal a tumour necrosis factor-related activation induced cytokine
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ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG
                                  GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTTGGGCCAAGATCTCCA 467
                                                                  GCT--CATAAAACGAGTCTTTCTTCGTTGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                     GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG 407
                                                                                                                                                                         181;
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/*tag= b
/note= "Target region for 95..829
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    member 11 (TNFSF11), Specifically claimed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product=
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                                                                                                                                                                                        46.48;
74.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splice variant
                                                                                                                                                                       0
                                                                                                                                                                                                        Score 121.2;
                                                                                                                                                                                        Pred. No.
                                                                                                                                                                      Mismatches
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RESULT 10
ABK12876
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   TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy; bone damage; cartilage damage; traumatic injury; surgery; osteoarthrit rheumatoid arthritis; acromegaly; gigantism; exostosis; carilaginea; exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;
having a disorder comprising insufficient or excessive cartilage or skeletal growth, where the disorder comprising insufficient cartilage or skeletal growth is selected from dwarfism, osteopetrosis,
                                                                                The present invention relates to a new method of treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth. The method of the invention involves administering to
                                                                                                                                                                                                      cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor-related activation induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA encoding human TRANCE protein splice variant 1
                                                  the mammal a tumour necrosis factor-related activation induced cytoki (TRANCE)-modulating agent. The method is useful for treating a mammal
                                                                                                                                                                                                                                                                                                                        Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK12876 standard; cDNA; 2226 BP
                                                                                                                                                     Disclosure; Fig 1; 55pp; English.
                                                                                                                                                                                     cytokine-modulating agent to mammal -
                                                                                                                                                                                                                                      Treating mammal having disorder characterised by abnormal
                                                                                                                                                                                                                                                                                           WPI; 2002-304119/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Tumour necrosis factor (ligand) superfamily, member 11 (TNFSF11), target region for antis nucleic acid. Specifically claimed in claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product=
                                                                                                                                                                                                                                                                                                                            Marks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Human TRANCE (tumour necrosis factor-related
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Best Local
WPI; 2000-271444/23
                                                             Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   craniofacial-skeletal discrepancies and bone or cartilage damage resulting from traumatic injury, surgery, osteoarthritis or rheumatoid arthritis, and discrepances comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, carilaginea, exostosis bursata and multiple osteocartilaginous exostoses. The method is useful for inhibiting chondrocyte differentiation. The present nucleic acid sequence encodes the human TRANCE protein, splice variant 1, of the invention. TRANCE is a member of the tumour necrosis factor
                                                                                                                                                                                    15-SEP-1998;
02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                             WO200015807-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding a human osteoprotegerin ligand (OPGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUL-2000
                                                                                                                       (MEBI-) M & E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ99964 standard; DNA; 2271 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2226 BP; 656 A; 448 C; 505 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family and acts directly on cartilage-producing cells (chondrocytes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCT--CATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TA 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      response; osteoporosis; bone resorption; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                             Haaning J;
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                                                                                                                       BIOTECH AS
                                                                                                                                                                                    98DK-0001164.
98US-0102896.
                                                                                                                                                                                                                                                                            99WO-DK00481
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "osteoprotegerin ligand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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74.88;
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Pred. No. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1e-30;
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Best Local
               W09846751-A1
                                                                                                                                                                                             Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a human osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL occurrentiation of animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                                                                                            Homo sapiens
                                                                                                                                                                                   Paget's
                                                                                                                                                                                                                                                                         Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert
                                                                                                                                                                                                                                                                                                                                                                                              AAV70285 standard; DNA; 2274
                                                                                                                                                                                                                                                                                                                    11-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2271 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide or subsequence, and/or at least one OPGL analogue to induce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 GCT--CATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vivo down-regulation of osteoprotegerin ligand (OPGL) activity used treat, prevent and ameliorate osteoporosis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC 235
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                                                                                                                                                                                   disease; ss.
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                                                                                     Location/Qualifiers 185..1138
                                                /product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.4%;
                                              "osteoprotegerin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Pred. No. 2.1
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Best Local S
Matches 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding OPG binding protein are used to produce recombinant OPG binding protein. OPG binding protein is used in binding assays to determine osteoprotegrin (OG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful in immunoassays for detection of OPG binding protein) and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding OPG binding protein can be used to detect OPG binding protein-encoding sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for antisense regulation of OPG binding protein expression. Modulators of OPG binding protein, particularly soluble forms of OPG binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation and for diagnosis {\sf Constant}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-1998;
16-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-594578/50
P-PSDB; AAW83195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, loosening of prostheses,
 ABK40274;
                                   ABK40274 standard; cDNA; 2390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     optionally in combination with agents that promote bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes human osteoprotegerin (OPG) binding protein. Host cells transfected with vectors containing nucleic acid molecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
                                                                                                                        T A -
                                                                                                                                                                                                                                                                                                                                                                      GCT--CATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                           GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG 716
                                                                                                                                                         TA
                                                                                                                                                                                                                CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC
                                                                                                                                                                                            CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC
                                                                                                                                                                                                                                                                  ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG
                                                                                                                                                                                                                                                                                                    ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG
                                                                                                                                                                                                                                                                                                                                       GTTCCCATAAAGTGAGTCTGTCCTTTGGTACCATGATCGGGGTTGGGCCCAAGATCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181;
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97US-0842842.
97US-0880855.
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74.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.1e
); Mismatches
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                                                                                            Matches
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Best Local
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22-JUN-1999;
20-JUL-1999;
26-JUL-1999;
28-JUL-1999;
17-AUG-1999;
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15-SEP-1999;
30-NOV-1999;
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11-MAR-1999;
11-MAY-1999;
                                                                                                                                                                                                polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc.), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immune disorder; angiogenic disorder; gene therapy; cytostatic; neuroprotective; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                   Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-1999;
01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                            The present invention relates to the isolation of novel human PRO
                                                                                                                                                                                                                                                                                                                                                       Claim 50; Fig 41; 302pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    malignancies, inflammatory, angiogenic and immunologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-AUG-1999;
                                                                                                                                                     Sequence 2390 BP; 778 A; 417 C; 506 G; 688 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAU86148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marsters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ashkenazi AJ,
                                                                                                                                                                                   polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                              778
 64 GCT--CATAAAACGAGTCTTTCTTCGTAGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                               4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding human PRO206 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002-205567/26.
                             GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG 837
                                                                                            181;
                                                                                                         Similarity
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000WO-US00219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goddard A,
Pan J, Pit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-146222P.
99US-149395P.
99US-151689P.
99WO-US20111.
99WO-US21090.
99WO-US28313.
99WO-US28301.
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99US-140653P
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99US-145698P.
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                                                                                                      46.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Godowski PJ,
i RM, Roy MA,
                                                                                          0; Mismatches
                                                                                                      Score 121.2;
Pred. No. 2.2
                                                                                                         2.2e-30;
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Smith V,
                                                                                                                         DB 24;
                                                                                            53; Indels
                                                                                                                       Length 2390;
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RESULT 14
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                                     The present sequence encodes human TNF-related activation induced cytokines (TRANCE). Human or murine TRANCE polypeptides or their variants, fragments, derivatives or analogues may be used as modulators of immune response in a mammal comprising, antisense sequences to TRANCE and fusion proteins comprising human and/or murine TRANCE. Agonists and antagonists of TRANCE, can be used to modulate immune response by increasing or decreasing the life span of mature dendritic cells and increasing or decreasing T cell activation. These techniques are especially useful for treating immune system related conditions such as HIV, cancer, autoimmune disease or hypersensitivity to an allergen. The TRANCE polypeptides can be used to increase the viability of dendritic cells in vivo or in vitro, especially when used in conjunction with proteins of the tumour necrosis factor (TNF) superfamily (especially rance-archan)
                                                                                                                                                                                                                                                                                                                                                                                                                11-DEC-1998;
12-DEC-1997;
03-MAR-1998;
Sequence 1823 BP; 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANCE; tumour necrosis factor superfamily; signal transduction; TNF; TNF-related activation induced cytokine; immune response; cancer; autoimmune disease; HIV; hypersensitivity; allergen; ds.
                                                                                                                                                                                                                                                     Claim 1; Fig 1; 164pp; English.
                                                                                                                                                                                                                                                                            TNF like proteins for treating autoimmunity and cancer
                                                                                                                                                                                                                                                                                                                                                          Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
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                                 or TNF-alpha).
                                                                                                                                                                                                                                                                                                               AAY17873
                                                                                                                                                                                                                                                                                                                                                        Josien R,
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97US-0989479.
98US-0034099.
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380 G;

569 T; 0 other;

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Best Local Similarity
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The present sequence is the coding sequence for rat Osteoclast Differentiation Factor (ODF). ODF is thought to be directly involved in the differentiation of monocytes/macrophages into osteoclasts. Osteoclasts promote dissolution of the bone matrix and solubilisation of bone salts. The present sequence is useful in gene therapy, and as hybridisation probes or primers. ODF protein is useful for modulating the
                                                                                                       Claim 1; Fig 1; 81pp; English.
                                                                                                                                          Novel nucleic acid encoding rat osteoclast differentiation factor useful for modulating activity of a cell, e.g., cell proliferation
                                                                                                                                 cell differentiation and cell viability
                                                                                                                                                                                           P-PSDB; AAB82092.
                                                                                                                                                                                                                                    Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat; osteoclast formation inducer; vaccine; gene therapy; Osteoclast Differentiation Factor; bone; ss.
                                                                                                                                                                                                                                                                (UYWA-) UNIV WESTERN AUSTRALIA
                                                                                                                                                                                                                                                                                            29-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat osteoclast differentiation factor, ODF, coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
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                                                                                                                                                                                                                                    Zheng M;
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                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Rat ODF"
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74.0%;
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Pred. No. 2.3e-29;
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Search completed: December 8, 2002, 17:26:15 Job time: 81.3192 secs
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                                                                                                                                                                                                                                                     Query Match 39.1%; Score 102; DB 22; Length 957; Best Local Similarity 69.8%; Pred. No. 4.4e-24; Matches 169; Conservative 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                    activity of cells, e.g., cell proliferation, cell differentiation and cell viability, as immunogens to generate anti-rat ODF antibodies, and as vaccines. Anti-rat ODF antibodies are useful in assay methods for quantifying ODF polypeptides.
                                                                                                                                                                                                                                                                                              Sequence 957 BP; 230 A; 260 C; 256 G; 211 T; 0 other;
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Title:
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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REFERENCE

AUTHORS

Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A., Goddowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watanabe,C.K. and Wood,W.I.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ORGANISM

Homo sapiens

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result RESULT 1 AX358828 LOCUS DEFINITION ACCESSION VERSION ဂ ဂ SOURCE KEYWORDS იი a ŏ 249.4 249.4 121.2 121.2 121.2 121.2 121.2 121.2 121.2 Score 121.2 121.2 121.2 121.2 121.2 84.8 81.6 81.6 81.6 37.2 1186 bp Sequence 81 from Patent WO0193983. AX358828 AX358828.1 GI:18675315 human Match Length Query 96.2 96.2 95.6 95.6 37755122 377552 1186 165707 190748 2029 3 2029 3 276831 3 142588 3 143451 1 166759 113451 200724 754 169960 127812 1034 2201 2271 2390 864 951 951 951 951 1630 1630 1630 1694 2191 2191 DВ 00000000 10 ω 992220 10 10 10 10 10 10 AX358828 AX362321 AC104794 AR164148 AX147989 AB061227 AB037599 AC094149 E34349 AX451897 AR157058 E36388 AF01317 AL139382 AB064269 AB064270 AX451895 AR156434 AR062119 AX140162 E34350 AC023297 AX201362 AF053712 AF019047 AB064268 AR164147 AR156433 AX147987 AB032772 AF187319 ALIGNMENTS DNA linear AX451897 Sequence AX157058 Sequence AX140162 Sequence AF019048 Mus muscu AF013170 Mus muscu AF062119 Sequence AF053713 Mus muscu AB061227 AB037599 AR156434 AR164148 AX147989 AX451895 AB064270 AB064269 AB022039 Mus muscu AC126690 Mus muscu AC113992 Mus muscu AC023297 Homo sapi AC007716 Homo sapi AC104794 AC010969 Description AF019047 Homo sapi AF053712 Homo sapi AX201362 Sequence AF187319 Rattus no AB064268 AR156433 Sequence AR164147 Sequence AX147987 Sequence E34350 DNA and pro E36388 Novel prote AC023297 Homo sapi AL139382 Human DNA AX232589 Sequence AC094149 Rattus no E34349 DNA and pro AB032772 Mus muscu AC006440 Homo sapi AB008426 Mus muscu AB036798 Mus muscu PAT 13-FEB-2002 Sequence Sequence Sequence Sequence Sequence Sequence Homo sapi Homo Homo sapi Homo sapi Homo Homo sapi sapı

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Secreted and transmembrane polypeptides and nucleic acids encoding
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285 c 299 g 288
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100.0%; Pi
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                                                                                                                                                                              Sequencing vector: M13; 08
Sequencing vector: M13; 08
Sequencing vector: plasmid; 1008
Chemistry: Dye-primer ET; 08 of reads
Chemistry: Dye-terminator Big Dye; 1008 of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 162662 bases at least Q40
Consensus quality: 163189 bases at least Q30
Consensus quality: 164786 bases at least Q20
Insert size: 9479; agarose-fp
Insert size: 167795; sum-of-contigs
Quality coverage: 10.78 in Q20 bases; sum-of-contigs
Quality coverage: 10.53 in Q20 bases; sum-of-contigs
Quality coverage: 10.53 in Q20 bases; sum-of-contigs
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                   * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (30-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: H_NH0254F07
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
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as soon as it is available and the accession number will
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JOURNAL
                                                    AUTHORS
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                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                    AUTHORS
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                                                                                                                                                                     PUBMED
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                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens BAC clone RP11-95D17 from 2, complete sequence ACC010969
Waterston,R.H.

Direct Submission
Submitted (28-SEP-1999) Genome Sequencing Center, Washington
Submitted (28-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                 l (bases 1 to 190748)
Sulston, J. E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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                                                                                      Unpublished
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                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                     Sun, H., Abbott, A.
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                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                    The sequence of Homo sapiens BAC clone RP11-95D17
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76228
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76328. .165707
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42242 c 39083 g 41295 t
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/chromosome="2"
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1212: gap of unknown length
7627: contig of 75015 bp in length
76327: gap of unknown length
165707: contig of 89380 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                            190748 bp
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Waterston,R.H.
Direct Submission
Submitted (19-APR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                  мо 63108,
6 (bases
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5 (bases
                                                                                                                                                     Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63 on Apr 19, 2001 this sequence version replaced gi:11128441.
                                                                                                                                                                                                                                                                                                                                                                 Waterston,R.H.
Direct Submission
Submitted (20-APR-2001) Genome Sequencing Center, Washington
Submitted (20-APR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                              Direct Submission
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                                              Contact: sapiens@watson.wustl.edu
                                                                                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
Center project name: H_NH0095D17
                                                                             Web site: http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                     1 to 190748)
                                 Summary Statistics
                                                                                                                                                                                                                          63108, USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. Mapping information for this clone was provided by Dr. John D. Mapping information of Genetics, Washington University, St. Louis McPherson, Department of Genetics, Washington University, St. Louis McD. For additional information about the map position of this McD. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
source information:
SOURCE INFORMATION:
Accordance by Oscerawa K. Woon, P.Y., Zhao, B., Frengen, E.

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., danor, A., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://gac.med.buffalo.edu)

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-521D12. Actual start of this clone is at base position 1 of RP11-95D17; actual end is at base position 190748 of RP11-95D17.

There are polymorphic base differences between RP11-95D17 and the redundant clone AC062035. Data from AC062035 was used to finish RP11-95D17.

Unresolved tandem repeat from base position 181200 to 187300. Siz information from restriction digest suggests that the full repeat may not be represented.

FEATURES Location/Qualifiers
source 1..190748
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"

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repeat_region
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9322. .9647
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4196. .5255
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2626. .3646
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185. .230
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325. .805
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/clone="RP11-95D17"
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Db 174245 TGTAATTTGAG 174235
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                                                        AB064268
                                                                                                                                                                                                          Db 174365 AACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGAC 174306
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Homo sapiens hranki 3 mrNa for receptor activator of nuclear factor ABD64258
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13614. .14110
/note="similar to
13623. .14122
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/note="similar to
14851. .15156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to 13735. .13801
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14062. .14259
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13688. .13942
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13630. .14128
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Pred. No. 7e-68;
O; Mismatches 1;
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JOURNAL REFERENCE REFERENCE AUTHORS TITLE

SOURCE

ACCESSION VERSION KEYWORDS AUTHORS ORGANISM Ikeda, T. and Kuroyama, H. Ikeda, T., Kuroyama, H. and Hirokawa, K. Determination of human RANKL isoforms Unpublished Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. HOMO sapiens AB064268.1 GI:18143616 Homo sapiens cDNA to mRNA. bases 1 to 818)

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Submitted (02-MAY-2001) Tohru Ikeda, Graduate School, Tokyo Medical and Dental University, Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          578
                                                         Ikeda, T. and Kuroyama, H. Direct Submission
                                                                                                                                                                                                                                                                                                  AB061227.1 GI:16610212
                                                                                                                                                                                                                                                                                                                                  Homo sapiens mRNA for hRANKL
                                                                                                                 Unpublished
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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psgshkvslsswyhdrgwakisnwtfsngklivnQdgffyYlyaniCfrhhetsgdlat
gylqlwvyvtktsikipsshtlmkGgstkywsgnsefhfySinvGgffklrsgeeisi
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                                                                       Submitted (26-JAN-2000) Masazumi Nagai, Iwate Medical University School of Dentistry, Department of Biochemistry; 19-1 Uchimaru, Morioka, Iwate 020-8505, Japan (E-mail:mnagai@iwate-med.ac.jp, Tel:+81-19-651-5111(ex.4436), Fax:+81-19-654-4147)
                                                                                                                                                       Nagai,M., Kyakumoto,S. and Sato,N. Direct Submission
                                                                                                                                                                                                                                                                                              Cancer cells responsible
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun.
                                                                                                                                                                                                                                                                             encoding a secreted form of ODF/TRANCE
                                                                                                                                                                                                                                                                                                                   Nagai, M., Kyakumoto, S. and Sato, N.
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SWIDLAKRSKLEAQFFAHLTINATDIFGSSHKVBLSSWYHDRGWAKISNMTFSNGKLI
SWIDLAKRSKLEAQFFAHLTINATDIFGSSHKVBLSSWYHDRGWAKISNMTFSNGKLI
VNQDGFYYLYANICFRHHETSGDLATEYLQLMYYTKTSIKIPSSHTLMKGGSTKYWS
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/db_xref="taxon:9606"
                /organism="Homo sapiens"
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GEAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG 532
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                                                                                                                                                                                                         Patent:
                                                                                                                                                                                                                                    Anderson, D.M.
                                                                                                                                                                                                                                                                                Unknown
                                                                                                                                                                                                                                                                                                 Unknown
                                                                                                                                                                                                  Isolated DNA molecules encoding RANK-L Patent: US 6242213-A 12 05-JUN-2001;
                                                                                                                                                                                                                                                                 Unclassified
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239 c 227 q
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RIKQAFQGAVQKELQHIYGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDI
PSGSHKVSLSSWYHDRGWAKISNMTFSNGKLIVWQDGFTYLYANICFRHHETSGDLAT
EYLQLAWYYTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISI
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184 c 200 g 260 t 3 others
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95. .829
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/protein_id="BAA90488.1"
/db_xref="GI:6863048"
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/tissue_type="tongue"
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Pred. No. 2.8e-27;
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Pred. No. 2.8e-27;
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  Eukaryota; Metazoa;
Mammalia; Eutheria;
                              Homo sapiens
                                                                                   Sequence 12 from Patent WO0136637 AX147989
                                                                     AX147989.1 GI:14346964
                                                                                                               AX147989
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Dougall,W.C. and Galibert,L.
Receptor activator of NF-kappa.B
Patent: US 6271349-A 12 07-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown
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239 c 227 g
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Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Anderson, D.M. and Hughes, A.E.
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Sequence 5 from Patent WO0224896.
AX451895
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                                                                                                                                                               WO 0224896-A 5 28-MAR-2002;
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239 c 227 g 233 t
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                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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                    /codon_start=:
                                     /note="unnamed protein product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB064270 972 bp mRNA linear PRI 26-DEC Homo sapiens hRANKL 2-2 mRNA for receptor activator of nuclear factor kappa B ligand 2-2, complete cds.
                                                                                                                                                                                                                                                                        Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
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Mammalia; Eutheria; Primates;
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                                                                                                               /gene="hRANKL 2-2"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                              Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:toru.pbh2@med.tmd.ac.jp, Tel:81-3-5803-5176,
                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ikeda, T., Kuroyama, H. and Hirokawa, K. Determination of human RANKL isoforms
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/Protein_id="BaB79694.1"
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/db_xref="GI:18143619"
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EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYA
                                                                                                                                                                                         /gene="hRANKL 1"
81. .1034
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SWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISINWTESNCKLI
VNODGFYYLYANICFRHHETSGDLATEYLOLMVYVTKTSIKIPSSHTLMKGGSTKVWS
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a 219 c 249 g 234 t
                                                                                                                                                    /gene="hRANKL 1"
/codon_start=1
                                                                                                                               /product="receptor activator of nuclear factor
                                                                                                                                                                                                                                            /db_xref="taxon:9606"
                                                                                                                  igand
                                                                                                                                                                                                                                                               ′organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metazoa;
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Primates;
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Pred. No. 2.8e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΤA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCT--CATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181;
                                                                                                                                                                                                                          Submitted (13-AUG-1997) Molecular Biology, University St., Seattle, WA 98101, USA
                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                        growth and dendritic-cell functio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens receptor activator (RANKL) mRNA, complete cds
                                                                                                                                                                                                                                                                   Cosman, D., DuBose, R. and
                                                                                                                                                                                                                                                                                 Anderson, D.M.,
                                                                                                                                                                                                                                                                                                                 9367155
                                                                                                                                                                                                                                                                                                                                                                    A homologue of the TNF receptor and its
                                                                                                                                                                                                                                                                                                                                                                                               Anderson, D.M., Maraskovsky, E., Tometsko, M.E., Roux, E.R., Teep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
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derson,D.M., Billingsley,W., Dougall,W.,

nnRose,R. and Galibert,L.
                                                                                                                                                                                                                                                                                                                                                                                                                           malia; Eutheria;
(bases 1 to 2201)
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/protein_id="AAB86811.1"
/db_xref="GI:2612922"
                           /product="RANKL"
                                                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NICFRHHETSGDLATEYLQLMYYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSIN
VGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID"
a 257 c 265 g 237 t
                                                                                   /gene="RANKL"
                                                                                                /gene="RANKL"
129. .1082
                                                                                                                                          /map="13q14"
                                         codon_start=1
                                                                     /note="receptor
                                                                                                                                                          /chromosome="13"
                                                                                                                                                                                    /organism="Homo
                                                                                                                                                                                                                Location/Qualifiers
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74.88;
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No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                            Billingsley,W.L., De,M.C., DuBose,R.F.,
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of nuclear factor kappa
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.8e-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCT -- CATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181;
                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 2271)
Lacey,D.L., Timms,E., Tan,H.-L., Kelley,M.J., Dunstan,C.R.,
Burgess,T., Elliott,R., Colombero,A., Elliott,G., Scully,S.,
Hsu,H., Sullivan,J., Hawkins,N., Davy,E., Capparelli,C., Eli,A.,
Qian,Y.-X., Kaufman,S., Sarosi,I., Shalhoub,V., Senaldi,G., Guo,J.,
Delaney,J. and Boyle,W.J.
Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
Cell 93 (2), 165-176 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens osteoprotegerin ligand mRNA, complete cds. AF053712
                                                                                                                                                                                                                                          One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                               Boyle,W.J
                                                                                                                                                                                                                                       mitted (16-MAR-1998) Department of Cell Biology, Amgen, Amgen Center Drive, Thousand Oaks, California 91320, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               658
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                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
185. .1138
                                                                                       activation"
/product="osteoprotegerin ligand"
/protein_id="AAC39731.1"
/db_xref="GI:3057146"
                                                                                                                                                                                                                   Location/Qualifiers
                                                              /codon_start=1
                                                                                                           /function="regulates osteoclast differentiation
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EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGMAKISNMTFSNGKLIVNQDGFYYLYA
NICFRHHETSGDLATEYLQLMYYTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSIN
VGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID"
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Copyright (c) 1993 - 2002 Compugen Ltd.
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6955 UI-1	BM66695	<u>ц</u>	w	3.4	39.2	39
3653 Pan	AG17365	17	\vdash	3.4	9	38
2337 UI-I	BQ18233	14	8	3.4	9	37
9542 QV4	AW74954	10	4	3.4	9	36
905 qi42	AI201905	9	412	3.4	9	35
5966 ES	AW97596	10	\sim	3.4	9	34
0697 AGE	BQ0	14	K 1	3.4	9	3
0767 DI	CNS005T	17	10	3.4	9	32
)150 RI	AQ49015	17	10	3.4	9.	3
1027 QV1	BE08102	10	4	•	9	30
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3573 HS_	AQ74357	17	\sim		40	28
1560 Pan	AG15456	17	\sim		40	27
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243 qi02g0	AI28	9	4			23
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3505 RP	AQ5:	17	-	•		21
2682 HS	AQ14268	17	$^{\circ}$	•		20
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L625 Te1	CNS03FF	17	vo.	•		17
497 RS:	BG20649	12	vo-	•	41.8	16
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ALIGNMENTS

COMMENT	TITLE JOURNAL	JOURNAL REFERENCE AUTHORS	TITLE	REFERENCE	SOURCE	AGCESSION VERSION VERSION KEYWOODS
(E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.	Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical Submitted Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Verbaue 200-0045, Tanan	<pre>Unpublished 2 (bases 1 to 659) Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,</pre>	Totoki, Y., Watanabe, H. and Sakaki, Y. BAC end sequences of Library PTB	<pre>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; EuteLeoscomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. 1 Fujivama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,</pre>	Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-112G09.F. Pan troglodytes	AG107545 659 bp DNA linear GSS 03-NOV-2001 Pan troglodytes DNA, clone: PTB-112G09.F, genomic survey sequence. AG107545 AG107545.1 GI:16728063

Result

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

<u>8</u>

Score

Match Length DB

ID

Description

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95.8 84.8 75.8 46.4 46.4

8.3 7.3 6.5 4.1 3.8

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AG107545 Pan trog1 BH267783 CH230-186 AV653073 AV653073 BF724774 bx08e07.y B92778 CIT-HSP-216 AA337226 EST42291

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143;
                                                                                    9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pleter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
Clones may be purchased from BACPAC Resources
                           (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html plate: 186 row: C column: 1
                                                                                                                                                                                                                                                                    Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                      Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Other GSSs: CH230-186C1.TJ
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1 (bases 1 to 612)
2hao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn
2 Cohregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F.,
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                      ,A., Gebregeorgis,E., Overton,L.,
Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library
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/clone_lib="PTB Chimpanzee Male BAC Library"
/168 c 121 g 189 t
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/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        603 TCTCTCTAGGTTCCCATAAAGTCAGTCTGTCCTCTTGGTACCATGATCGAGGCTGGGCCA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            538 TATCCCATGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAA 597
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hes 132;
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                                                                                                                                                                                                                                                                                                                                  Contact: Zeguang Han
Chinese National Human Genor
351 Guo Shoujing Road, Zhan,
201203, p. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCTGTACGCCAACATTTGCTTCAGGCATCATGAAACCTCAGGGAGCGTACCTGCGGACT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu, X., Huang, J., Xú, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.

Insight into hepatocellular carcinogenesis at transcriptome level by a communication of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: hanzg@chgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV653073.1 GI:9874087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                             clone is available at CHGC in
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCDHB01"
                                                                                                                                                                                                   1. .362
/tissue_type="corresponding non cancerous liver tissue"
                                             /clone_lib="GLC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="vector: pTARBAC2.1; Site_1: EcoRI; Site_2: E
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced
Pieter de Jong"
145 c 133 g 166 t
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/clone="CH230-186C1"
/clone_11b="CHORI-230 Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="BN/SsNHsd/MCW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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69.5%;
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Pred. No. 2.4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Center at Shanghai Zhangjiang Hi-Tech Park,
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GLCDHB01 3', mRNA sequence.
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bx08e07.y1 Human Iris cDNA (Un-normalized, unamplified): BX Homo sapiens cDNA clone bx08e07 5', mRNA sequence.
BF724774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 598)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: graeme@helix.nih.gov
Plate: 08 row: e column: 07
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Section on Molecular Structure and Function National Eye Institute
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301 496 0078
/note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris
tissue was pooled from 10 individuals ranging in age from
4-80 years and RNA was extracted. From this pooled sample
an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
directionally cloned cDNA library in the pCMVSPORT6 vector
was constructed at Life Technologies, essentially
following the protocols of the SuperScript Plasmid System
full details of which are contained in the manufacturer's
Instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adapter [5'-pGACTAGTTCTAGATCGCGAGCGCCCC(T)15-3'
]. Not I/blunt end inserts were cloned into the Not I/EcoR
V sites in the vector. EST analysis was performed on the
unamplified library at the NIH Intramural Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH, Bethesda, MD 20892-2740, USA
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XhoI"
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/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="bx08e07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Iris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Human Iris cDNA (Un-normalized, unamplified):
                                                                                                                                                                                                                                                                                                                                                                   /lab_host="EMDH10B"
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71.5%;
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Pred. No. 8.2e-11;
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182 GTGCCCACTATGCACCAGGCAATGTATATGATTCTAGAATTCAGCAACGAACAAGACAGA 123
                                                                                       349 GTATCTACAAGGCACCAGGCATTTTTTGAGCATTTGGGGATTTGTCAGCAAACAAGTCAGA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 AGTGTCTACTGTGTACTAGGGATTGTTCTAGCGGCTGGGATATAGCAGTAAACAAGGCAG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 GCAAAAATCCCTGACCTCATGGAACTGACCTTCTAG 1
                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B92778 487 bp DNA linear GSS 25-JUN-1991
CIT-HSP-2164D13.TR CIT-HSP Homo sapiens genomic clone 2164D13, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
Other_GSSs: CIT-HSP-2164D13.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linne Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simon, M. and Venter, J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 487)
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1 142 c 146 g
                                                                                                                                                                                                                              HindIII"
                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="2164D13"
                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:7100687"
                                                                                                                                                                                                                                                                                                                                                                                            1. .487
                                                                                                                                                                                                                                                                                                     /clone_lib="CIT-HSP"
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                                                                                                                                                                                                                                                                  /cell_type="Sperm"
                                                                                                                                                                                                                                                                                    /sex="Male"
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                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                        CATTITITGAGCATTTGGGATTTGTCAGCAAACAAGTCAGACAAAAAAACCTTGCTCTGGT 427
                                             CTTGTTCTAGGCACTTGGGATTCACCAGTATACAATGGAGACAAAAATCCCCTGCCCTGGA 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kerlavage, AR Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Index (http://www.tigr.org/tdb/hgi/hgi.html)
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                                                                                                                                               Conservative
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78 c 104 g 83 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="ATCC (inhost):139297"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                             /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Endometrial tumor"
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Pred. No. 0.13;
                                                                                                                                               Mismatches
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BASE COUNT
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                         Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 407)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                 AQ085343
407 bp DNA linear GSS 26-AUG-19:
HS_2164_B1_B07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2164 Col=13 Row=D, DNA sequence.
                                                                            Sequence-tagged connectors: A sequence approach to mapping and
                                                                     scanning the human genome
                                                                                                                                                                                                                                               Homo sapiens
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Contact: John Quackenbush
The Institute for Genomic Research
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Plate: 224
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., Q1,R., Abernathy,K., Dharap,S., Gaspard,R.,
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                                                                                                                                                                                                                                             Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Fax: (206) 616-3887
Email: jwallace@u.washington.edu
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University of Washington
401 Queen Anne Avenue North, Seattle,
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
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/db_xref="taxon:9606"
           /plasmid="pBeloBAC11"
/note="end : SP6"
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                                                                             /clone_lib="DrosBAC"
                                                                                                                      /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MMNMMMNNNMGGKGTTKMMMVMGMGGMKGKMGKHKKMGMGVGKGTKMTMCGGMMGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNMTNMNNNNNNMNMMNNNNNNNNNNNNNNTTTTTTTMMCTTHMTHMTMTHMMTTTHMTM 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMT NNT MMNNT NNN NMMMMMMMNT MMN MN NMMMMMMT C NMN MAT MMT MNG MN MN MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTGMGTMTTNGTTMTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KMSSGGMMGMMVGGSGGVSGCGGVMGGGGKSGGMMKKMKGYGTMMGGMVGGGGGGGBMGM 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAACTATGTAACCAGCATTGGGGTTGGGTGCCAGAGATCCAAAGCTAAGACACCAAAACC 812
                                                                                                                                Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random activation of gene expression
                                                                                                                                                                                                                                                                                                                                                                                                   BG197160
RST16397
                                                                                   Contact: Scott J. Cain
                                                                                                                                                                                                                                     1 (bases 1 to 198)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D.,
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Email: scain@athersys.com
                                                                  Athersys,
                                                                                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  BG197160.1
                                                                                                                                                                                                                                                                                                                                                                                  BG197160
                                                                                                                                                                                                                                                                                                                                human
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                1 Carnegie Ave, (
: 216 431 9900
: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 148; Mismatches
                                                                                                                   Biotechnol. 19 (5),
                                                                                                                                                                                                                                                                                                                                                                                                   Athersys RAGE Library
                                                                                                                                                                                                                                                                           Eutheria; Primates;
                                                                  Inc.
                                                                                                                                                                                                                                                                                                                                                                  GI:13718847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.8%;
11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            807
                                                  Cleveland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43.6; DB 17; Pred. No. 0.23;
                                                                                                                     440-445
                                                                                                                                                                                                                                                                                                                                                                                                                     198
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                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                     (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                   sapiens cDNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                           Perry, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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FEATURES

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465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
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                                                                                                                                                                                                                                                           401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 438)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ669724 438 bp DNA linear GSS 24-JUN-1999 HS_5381_A1_F01_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=957 Col=1 Row-K, DNA sequence. AQ669724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC, Hood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 148.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

3 56 c 41 g 46 t
                        /db_xref="taxon:9606"
/clone="Plate=957 Col=1 Row=K"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="See 'Creation of Genome-wide Protein Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43.4; DB Pred. No. 0.16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO.
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LOCUS
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                                                                                                                                                                                                  BASE COUNT
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Best Local S
Matches 59
                                                                                          Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                       source
                           363 CCAGGCATTTTTGAGCATTTGGGATTTGTCAGCAAACAAGTCAGACAAAAAAACCTTGCT 422
163 CCAGATATATTGTAGGCACTGAGGATATAGTGGTGAACAAAACAGGTGATCATCCTTGCC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTGTGGAGCTTACATTCTAAAATA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGTGGAGGGAACATTCTAGCAAA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAGCATTATTCTAGGCACTTGGGATATATCAGTGAACAAAACAGACAAAAATCCCTGTC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGGCATTTTTTGAGCATTTGGGATTTGTCAGCAAACAAGTCAGACAAAAAACCTTGCT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clones are availabe from end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ013160 355 bp DNA linear GSS 06-JUN-19 CIT-HSP-2298M3.TF CIT-HSP Homo sapiens genomic clone 2298M3, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
Mammalia; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ013160.1 GI:3185725
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301 838 0208
                                                                                        Conservative
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                                                                                                                                                                                           /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
67 c 83 g 92 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Yector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

87 c 62 g 122 t 1 others
                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:7153855"
/db_xref="taxon:9606"
/clone="2298M3"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                    /sex="Male"
                                                                                                                                                                                                                                                                                                          /clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metazoa;
                                                                                                          3.7%;
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Primates;
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                                                                                                        Score 43.2; DB Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43.4; DB Pred. No. 0.21;
                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                 DB
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RESULT 11 AQ669724

DEFINITION

VERSION

AQ669724.1 GI:5202558

SOURCE KEYWORDS ACCESSION

ORGANISM

Homo sapiens

δð В δ

525

TTAATACCATCAATATCCCATGAGG 549 TTAATGCCACCGACATCCCATGTGG 56

80

BASE COUNT ORIGIN

þ

Query Match Matches

Local

Similarity

3.7%;

Conservative

0

REFERENCE AUTHORS

COMMENT

JOURNAL MEDLINE TITLE

Proc.

scanning the human

genome

FEATURES

http://www.htsc.washington.edu Plate: 957 row: K column: 1 Seq primer: SP6

Class: BAC ends

quality sequence stop: Location/Qualifiers

source

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RESULT 13
BG940945
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TITLE
                                                                                                   Query Match
Best Local
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381 TTTGGGATTTGTCAGCAAACAAGTCAGACAAAAAACCTTGCTCTGGTGGAGGGAACATTC 440
                                                                            Local Similarity les 67; Conserv
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Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.
Gene expression in proliferating human erythroid cells
Genomics 59 (2), 168-177 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG940945
384 bp mRNA linear EST 11-JUN-ax08d07.x2 Proliferating Human Erythroid Cells (LCB:ax library) Homo sapiens cDNA clone ax08d07 random, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301 402 2373
Fax: 301 435 5148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Intramural Sequencing Center (NISC).
Plate: 08 row: d column: 07
Seq primer: -21M13 forward primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing and analyses by National Institutes of Health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: jm7f@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99339981
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BG940945
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                                                                                                                                                                                                       152
                                                                               Conservative
                                                                                                                                                                                     Site_2: ECORI; 65,000 proliferating erythroid cells from the buffy coat of a blood donation were obtained by flow cytometric separation after a 5-day culture period in the presence of erythropoietin. Total RNA was purified from the sorted cell population using TRIZOL reagent. RNA (0.3 ug) was converted into double stranded cDNA using Clontech's Capfinder cDNA Library Construction Kit (Clontech) according to the manufacturer's protocol and cloned into EcoRI digested Lambda Zap II vector (Stratagene). The phage library was amplified once prior to in vivo excision in SOLR cells. Individual colonies were grown, and the cDNA inserts were sequenced in high throughput (NIH intramural sequencing center http://www.nisc.nih.gov/)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood Mononuclear Cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: blood; Vector: Lambda ZAP II; Site_1: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="SOLR"
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                                                                                                   3.7%;
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                                                                                                   Pred. No. 0.39;
                                                                                                                        Score 42.4; DB 13;
                                                                          Mismatches
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RESULT 15
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                                                        314 TAATAAATATACTACATTAGAA 335
                                                                                                                                                                                                                                        346 CAAGTATCTACAAGGCACCAGGCATT-TTTTGAGCATTTGGGGATTTGTCAGCAAACAAGT 404
                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                               CAGGAGAAGTATTTGCTAAGAA 486
                                                                                                                            CGAGCACTTACTGTACACCAGGCATTGTTCTAGGTATATGAGATTCATTAACAAACTAAA 253
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                                                                                                                                                                                                                                                                               86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
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Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-018005.TJ.
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R.Site 2 : EcoRI
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                                                                                                                                                                                                                                                                                                                                                                          /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chim
192 c 79 g 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Pan troglodytes"
/db_xref="taxon:9598"
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206 t 3 others
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AUTHORS
Search completed: December Job time: 2585.48 secs
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Matches 58; Conserv
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21227151
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
Email: scain@athersys.com
High quality sequence stop: 276.
Location/Qualifiers
10276
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 276)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, R., Whittington,
T-in State of the Property of
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Creation of genome-wide protein expression libraries using random activation of gene expression

activation of gene expression

Nat. Bjotechnol. 19 (5), 440-445 (2001)
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BG203357
BG203357.1
GI:13725044

276 bp mRNA linear EST 21-APR-2
mRNA_linear EST 21-APR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.6%;
68.2%;
                                                         8, 2002, 19:26:54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1161
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Gapop 10.0 , Gapext 1.0
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1: \SIDS2/gcgdata/geneseq/geneseqn-emb1/NA198.DAT:*
2: \SIDS2/gcgdata/geneseq/geneseqn-emb1/NA198.DAT:*
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Copyright (c) 1993 - 2002 Compugen Ltd
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7908.746 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

9	8	7	σ	տ	4	ω	2	_	Result No.
126	126	126	126	126	126	126	126.2	268	Score
10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	23.1	Query Match Length DB
1945	954	954	954	954	954	954	741	1186	Length
24	22	22	22	19	19	19	19	24	
ABK12877	AAD05904	AAD08715	AAD15311	AAV41372	AAV41378	AAV69887	AAV69899	ABK33576	ID
cDNA encoding huma	Human full-length	Human receptor act	Human receptor act	NF-kB receptor act	NF-kB receptor act	Nucleic acid encod	Nucleic acid encod	cDNA encoding huma	Description

Human reproductive	AAL00215 AAH34950	22	983 983		44	4 4 4	
Human GLCL related	AAH51308	21	1001	3.9	45	43	C
Human GLCL related	AAH51592	21	1000		46.2	42	a
DNA encoding osteo	AAZ99973	21	519	٠		41	
DNA encoding osteo	AA299971	21	546	6.4	73.8	40	
ő	AAZ99970	21	564	6.4	74	39	
DNA encoding a syn	AAZ99967	21	564	6.4		38	
DNA encoding osteo	AAZ99972	21	519	6.4	74.2	37	
מ	AAZ99969	21	519	6.4	74.2	36	
DNA encoding a syn	AAZ99968	21	519		74.2	35	
	AAA39155	21	2029	7.0	81.6	34	
Mouse cDNA encodin	AAS13369	22	522	8.1	94.4	33	
DNA encoding a mur	AAZ99966	21	2299	8.4	97	32	
Human osteoprotege	AAV70284	19	2295	8.4	97	31	
cDNA encoding mous	ABK12880	24	2237	8.4	97	30	
Murine TRANCE enco	AAX80224	20	2237	8.4	97	29	
Nucleotide sequenc	AAV41489	19	2191	8.4	97	28	
Murine RANKL (rece	AAD05903	22	1630	8.4	97	27	
Murine receptor ac	AAD08714	22	1630	8.4	97	26	
	AAD15310	22	1630	8.4	97	25	
NF-kB receptor act	AAV41371	19	1630	8.4	97	24	
NF-kB receptor act	AAV41377	19	1630	8.4	97	23	
	AAH25526	22	1574	8.4	97	22	
Nucleic acid encod	AAV69886	19	1538	8.4	97	21	
Osteoclast formati	AAZ49024	21	951	8.4	97	20	
DNA encoding a mur	AAZ99965	21	951	8.4	97	19	
Mouse OBM nucleoti	AAA39156	21	951	8.4	97	18	
Nucleotide sequenc	AAV69900	19	951		97	17	
Nucleic acid encod	AAV69898	19	735	٠	97	16	
Rat osteoclast dif	AAF86481	22	957		102	15	
Human TRANCE encod	AAX80223	20	1823	•	122.8	14	
cDNA encoding huma	ABK40274	24	2390	•	126	13	
Human osteoprotege	AAV70285	19	2274	10.9	126	12	
DNA encoding a hum	AAZ99964	21	2271		126	11	
cDNA encoding huma	ABK12876	24	2226	10.9	126	10	

ALIGNMENTS

PR	PR	PR	PR	PR	PR	PR	PR	ЭF	XX	X X	PN	XX	SO	XX	ΚW	ΚW	KW	KW	××	DE >	¥ F	×	AC	××	ij	ABK33576	RESU
25-JUL-2000; 2000US-220666P. 26-JUL-2000; 2000US-220893P.	25-JUL-2000; 2000US-220664P.	25-JUL-2000; 2000US-220638P.	25-JUL-2000; 2000US-220624P.	25-JUL-2000; 2000US-220607P.	25-JUL-2000; 2000US-220605P.	25-JUL-2000; 2000US-220585P.	20-JUL-2000; 2000US-219556P.	29-JUN-2001; 2001WO-US21066.		31-TAN-2002	WO200208288-A2.		Homo sapiens.			~		Human; secreted protein; PRO; tumour; lung cancer; colon cancer;	•	cDNA encoding human PRO protein, Seq ID No 81.	08-MAI-2002 (IIISC entry)		ABK33576;		ABK33576 standard; cDNA; 1186 BP.	3576	LT 1

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                                                                                                                                                                                                                                                                                                                                                                                                       CC The invention relates to one hundred and twenty two nucleic acids CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides CC encode human secreted proteins. The PRO nucleic acids, polypeptides, CC agonists and antagonists are useful for treating a PRO related disorder. CC The PRO polypeptides are useful for diagnosing tumours, especially lung CC cancer, colon cancer, breast tumour, prostate tumours, rectal tumour or CC liver tumour. The PRO polypeptides are useful for stimulating the CC the proliferation of, or gene expression, in pericyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for CC timulating the release of tumour necrosis factor-alpha from human blood, CC for stimulating or inhibiting the proliferation of normal human dermal CC weight markers and for tissue typing. The PRO nucleic acids have CC applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABK33536-ABK33657 represent human CC PRO protein coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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23-AUG-2000;
24-AUG-2000;
15-SEP-2000;
10-NOV-2000;
28-NOV-2000;
01-DEC-2000;
20-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
                                                                                                                                                                                                                                                                                                                                                                               Sequence 1186 BP; 314 A; 285 C; 299 G; 288 T; 0 other;
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                                                                                                                                                                                                       AGGACCTTCAGCTATGGTGTAATTTGAG
                               AGGACCTTCAGCTATGGTGTAATTTGAG 736
                                                            ATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGC
                                                                                        ATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGC
                                                                                                                         ATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTT
                                                                                                                                          ATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTT
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DB; AAU83632.
                                                                                                                                                                                                                                                                                                                       268;
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                                                                                                                                                                                                                                                                                                                                      Similarity
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C, Gurney
                                                                                                                                                                                                                                                                                                                   23.1%; Score 268; DB 24; ilarity 100.0%; Pred. No. 3.6e-76; Conservative 0; Mismatches 0;
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2001WO-US06520.
2001US-0854280.
2001WO-US17092.
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2000WO-US233522
2000WO-US233528
2000US-000000P
2000WO-US30873
2000WO-US3646P
2000WO-US32678
2000WO-US32678
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 697
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Stephan
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Best Local
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                                                                                                                                                                                                          (OCIF) binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (sOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein for investigation and allocation metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUN-1997;
12-AUG-1997;
21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the
                                                                                                                                                                                                                                                                                                                                                                                                                               for, e.g. treatment calcium metabolism
                                                                                                                                                        Sequence 741 BP; 230 A; 153 C; 158 G;
                                                                                                                                                                                                   of the protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and
                   465
                                                                                                                                                                                      components
                                                                                                                                                                                                                                                                                                                                                                                                     Example 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goto M,
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15-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic
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                                                                     -CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTT 523
                                          GAATTACAACATATCGTTGGATCACAGCACATCAGAGCAGAGAAAGCGATGGTGCATGGC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss.
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                                                                                                                  Similarity
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N, Yamaguchi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N, Shima N,
                                                                                                                                                                                      of drugs.
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                Pages 121-122; 151pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bone
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97JP-0097808.
97JP-0151434.
97JP-0217897.
97JP-0224803.
                                                                                                                                                                                                for investigative and diagnostic purposes, and
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1..741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   absorption factor; bone disorder; calcium metabolism;
                                                                                                                 10.9%;
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Takahashi K,
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                                                                                                               Score 126.2; DB 1
Pred. No. 3.8e-30;
                                                                                                  Mismatches
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Tomoyasu A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yasuda H;
                                                                                                                                                          200 T; 0 other;
                                                                                                                            DB 19;
                                                                                                  93;
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Tsuda E;
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The present sequence encodes an osteoclastogenesis inhibitory factor (OCIF) binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane protein then affinity chromatography using OCIF. It exists in a full-sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM osteoclast; bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid
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                                                                                                                                                                                                                                                                                                                                                    09-JUN-1997;
12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; ss.
                                                                                                                                                           Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and
                                                                                                                                                                                                                                                Nakagawa N, Shima N,
Washida N, Yamaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                            15-APR-1998;
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                                                                                                                    Claim 38; Page 115; 151pp; Japanese
                                                                                                                                                 calcium metabolism
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                                                                                                                                                                                                                                                                                                         (SNOW ) SNOW BRAND MILK PROD CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCA 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAAT 414
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                                                                                                                                                                                                                                                                Higashio K,
N, Shima N,
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97JP-0097808.
97JP-0151434.
97JP-0217897.
97JP-0224803.
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K, Yano K, Yasuda H;
                                                                                                                                                                                                                                                                            Kobayashi F,
                   membrane proteins
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Best Local
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                                                                                                           14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       components of drugs.
                                                                                                                                                                                                                                                                                                                                                    RANKL; RANK ligand; tumour necrosis factor; TNF; ss
                                                                                                                                                                                                                                                                                                                                                                                                         NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV41378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV41378 standard; cDNA;
                                                                                                                                                                                            02-JUL-1998.
                                                                                                                                                                                                                        W09828426-A2
                                                                                                                                                                                                                                                                                                                          Homo sapiens
             P-PSDB; AAW69957
                          WPI; 1998-377657/32
                                                     Anderson DM,
                                                                              (IMMV ) IMMUNEX CORP.
                                                                                                                                                                  22-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                   necrosis factor-kappa B; NF-kB; receptor activator; human;
e response; inflammatory response; toxic shock; sepsis;
                                                                                                                                                                                                                                                                                                                                                                response;
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                                                                                                          97US-0064671.
96US-0059978.
97US-0813509.
                                                                                                                                                                  97WO-US23775
                                                                                                                                                                                                                                                    /product= "human RANKL (ligand for RANK)"
                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                     Maraskovsky
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AAV41372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                        RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
                                                                                                                                                                                                         NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                 AAV41372 standard; cDNA; 954 BP
                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                08-OCT-1998
                                                                                                                                                                                                                                                                                                           AAV41372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 954 BP; 255 A; 239 C; 227 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                           (first entry)
                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 126; DB 19;
Pred. No. 5.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      696
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AAD15311 standard; cDNA; 954 BP

AAD15311;

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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This cDNA encodes a human RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. Host cells transformed or transfected with an expression vector comprising the RANK encoding or transfected with an expression vector comprising the RANK encoding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       can also be used for detection and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7; Pages 59-60; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated receptor activator of necrosis factor-kappa | for, e.g. developing products for regulating an immune or inflammatory response, treating toxic shock or sepsis
                                                                                                              697
                                                                                                                                                                                                                          569
                                                                                                                                                                                                                                                               583
                                                                                                                                                                                                                                                                                                    509
                                                                                                                                                                                                                                                                                                                                                                             449
                                                                                                                                                                                                                                                                                                                                                                                                        465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-377655/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9828424-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-1998.
                                                                                                                                             AGGATGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                                                                                                                                                      ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA----
                                                                                                                                                                                                                                                                                                                   TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTCGAAACATG 582
                                                                                                                                                                                                                                                                                                                                                                   CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 508
                                                                       ACCTAGCTACAGAGTATCTTCAACTA 714
                                                                                                        GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                            TTAATGCCACCGACATCCCATCTGGTTCCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG 568
                                                                                                                                                                                   ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
                                                                                                                                                                                                                    ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Galibert LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0064671.
96US-0059978.
97US-0813509.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "human RANKL (ligand for RANK)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.9%;
72.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maraskovsky E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 126; DB 19;
Pred. No. 5.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 954;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful
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                                                                                                                                                                                 696
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CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member CC with TNF receptor associated factor (TNF) receptor superfamily and associates CC with TNF receptor associated factor (TNF)? 2 and 3 which are important CC in the regulation of immune and inflammatory response. The receptors CC are useful for regulating immune response and in screening for inhibitors of immune and inflammatory response. The receptors CC assays for inhibitors of signal transduction, e.g. for screening the CC assays for inhibitors of signal transduction, e.g. for screening the CC assays for inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, CC TRAF5 and particularly TRAF6. NF kappaB inhibition by RANK antagonists CC are useful in ameliorating the negative effects of an inflammatory CC response that result from triggering of RANK, e.g. in treating toxic reactions and the effects of bone rescription. RANK acts as an anti-CC apoptotic signal and rescue the cells that express RANK from apoptosis. CC soluble forms of the receptor are used in vivo or in vitro based CC screening tests for agonists or antagonists of RANK mediated NF-kappa B activation, or to inhibit CC transduction of a signal via RANK. RANK compositions are used in the CC express RANK. Compounds that interfere with RANK/TRAF6 interactions are useful for modulating the formation of osteoclasts from osteoclast form osteoclast fined activities. They are used in shibitors of diseases associated with express home rescription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; receptor activator of nuclear factor kappaB ligand; RANKL; NF; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF; immune response; inflammatory response; graft-versus-host reaction; toxic shock; sepsis; acute inflammatory reaction; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adjunct therapy for disease characterized by neoplastic cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 7; Column 69-71; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dougall WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-OCT-1997;
are used as inhibitors of diseases associated with excess bone resorption and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are useful for the expression of recombinant proteins, as probes for analysis of the presence or distribution of RANK transcripts, while the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    patent discloses novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-520313/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor activator of NF kappaB ligand (RANKL) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE08738
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96US-0772330.
97US-0813509.
97US-0996139.
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97US-0077181.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Human RANK ligand (RANKL) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor activator of nuclear factor (NF)
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AAD08715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
Matches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are useful in preparing kits for the detection of soluble RANK, or monitor RANK-related activity. The present sequence is a cDNA enco human RANK ligand (RANKL) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                           Human; receptor activator of NF-chi B; RANK; tumour necrosis factor; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human receptor activator of NF-chi B ligand (huRANKL) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD08715 standard; cDNA; 954 BP
                                                                                                                                   (IMMV ) IMMUNEX CORP.
                                                                                                                                                                           23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                         US6242213-B1.
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                                                                   P-PSDB;
                                                                              WPI; 2001-407216/43.
                                                                                                          Anderson
                                                                                                                                                                                                                   22-DEC-1997;
                                                                                                                                                                                                                                              05-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     509
                                                                                                                                                               14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 508
                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTTCCTTTGGTACCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTAGCTACAGAGTATCTTCAACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTAGCAATGGAAAACTAATAGTTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                   AAE04426
                                                                                                          DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                            96US-0059978.
97US-0077181.
97US-0064671.
                                                                                                                                                                                                                    97US-0995659
                                                                                                                                                                                                                                                                                                  /product= "Human RANKL protein"
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.9%;
72.6%;
                                                                                                                                                                                                                                                                                                               þ
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Pred. No. 5.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   628
                                                                                                                                                                                                                                                                                                                                                                                                  SS
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New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi B receptor activator) of the receptor activator of NF-chi B (RANK) -

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AADOS904
ID AADO
XX
AC AADO
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AC AADO
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SI Humma
KW Humma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
17-NOV-1999;
                                                           14-NOV-2000; 2000WO-US31459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; receptor activator of NF-kappaB; RANK; nuclear factor-KappaB; NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;
                                                                                                                                 25-MAY-2001.
                                                                                                                                                                                                WO200136637-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic; inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial expansile osteolysis; FEO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human full-length RANKL (receptor activator of NF-kappaB ligand) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD05904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD05904 standard; cDNA; 954 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to receptor activator of NF-chi B (RANK) DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---AAGGCATTTATTACCGGAATGCCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTAGCTACAGAGTATCTTCAACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
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   99US-0442029
                                                                                                                                                                                                                                        /product= "Human full-length RANKL (receptor activator
of NF-kappaB ligand) protein"
                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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18-JUN-2002 (first entry)

ABK12877 standard; cDNA; 1945 BP

Human; tumour necrosis factor-related activation induced cytokine; TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy,

cDNA encoding human TRANCE protein splice variant 2.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene-activating mutations, associated with e.g. familial expansile osteolysis (FEO) and early onset Paget's disease of bone (EP). The present sequence is a CDNA encoding full-length human RANKL (huRANKL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factors (TRAFs). Triggering of RANK by overexpression or co-expression of RANK and membrane bound RANK ligand (RANK) results in upregulation of the transcription factor NF-KappaB, a ubiquitous transcription factor that is most extensively utilised in cells of the immune system. Inhibition of NF-KappaB by RANK antagonists is useful in ameliorating negative effects of inflammatory reactions, and the effects of excess bone resorption. The RANK DNAs, proteins and their analogues are useful for the preparation of pharmaceutical compositions, for infecting target cells for use in Gene +hereny analogues in infecting target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells for use in gene therapy applications in diagnosing diseases associated with RANK, and as targets for use in screening assays. They may be used in the treatment or diagnosis of immune system dysfunction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein.
      689
                                                                                         629
                                                                                                                                                                                569
                                                                                                                                                                                                                                                                  509
                                                                                                                                                                                                                                                                                                                                                                                       465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (receptor activator of NF (nuclear factor)-kappaB), a member of TI (tumour necrosis factor) receptor superfamily. RANK is a Type I transmembrane protein that interacts with TNF receptor-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a novel receptor, referred to as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 75-76; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA encoding a receptor activator of NF-kappaB polypeptide for the treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson DM, Hughes
                                                                                                                                                                                                                         583
                                                                                                                                                                                                                                                                                                                                            449 CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                         GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                         TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG 568
ACCTAGCTACAGAGTATCTTCAACTA 714
                                                                                  AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                           ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                                                                                       ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC 628
                                                                                                                                                                                                                ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA--- 639
                                                                                                                                                                                                                                                                                                     TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
                                                                                                                                                                                                                                                                                                                                                                                                                                          193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention also encompasses gene therapy methods to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   located in chromosome 13q14.
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 126; DB 22;
Pred. No. 5.1e-30;
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                                                                                                                                                                                                                                                                                                                  having a disorder comprising insufficient or excessive cartilage or the mammal a tumour necrosis factor-related activation induced cytokine (TRANCE) modulating agent. The method is useful for treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth, where the disorder comprising insufficient cartilage or skeletal growth is selected from dwarfism, osteopetrosis, craniofacial-skeletal disorderancies and bone or cartilage damage resulting from traumatic injury, surgery, osteoarthitis or rheumatoid arthritis, and disorders comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, carilaginea, growth are selected from acromegaly, gigantism, exostosis, carilaginea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor-related activation induced cytokine-modulating agent to mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200216551-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-AUG-2000; 2000US-226197P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2001; 2001WO-US26101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2002
                                                                                                                                                                                                                                           exostosis bursata and multiple osteocartilaginous exostoses. The method is useful for inhibiting chondrocyte differentiation. The present nucleic acid sequence encodes the human TRANCE protein, splice variant 2, of the invention. TRANCE is a member of the tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating mammal having disorder characterised by abnorma
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                                                                                                                                                                                        Sequence 1945 BP; 623 A; 326 C; 392 G; 601 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 3; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT
                                                                                                                                                                                                                           family and acts directly on cartilage-producing cells (chondrocytes).
                                       324
 525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCGGAAACATG 582
                                                                           465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to a new method of treating a mammal
                                       CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 383
                                                                                                                                  Similarity
                                                                                                                Conservative
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note- "Target region for antisense nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Human TRANCE (tumour necrosis factor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Tumour necrosis factor (ligand) superfamily,
    member 11 (TNFSF11), Specifically claimed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                  10.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activation induced cytokine) protein, splice variant 2"
                                                                                                                                Score 126; DB 24; Length 1945; Pred. No. 7.7e-30;
                                                                                                                  Mismatches
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK12876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis; rheumatoid arthritis; acromegaly; gigantism; exostosis; carilaginea; exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK12876 standard; cDNA; 2226 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cartilage growth; skeletal growth; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding human TRANCE protein splice variant 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444 ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTAGCAATGGAAAACTAATAGTTAATC
                                                                                           cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor-related activation induced cytokine-modulating agent to mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            640 ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
                                                                                                                                      Treating mammal having disorder characterised by abnormal
                                                                                                                                                                                                                                                                18-AUG-2000; 2000US-226197P
                                                                                                                                                                                                                                                                                            20-AUG-2001; 2001WO-US26101
                                                                                                                                                                                                                                                                                                                                                   WO200216551-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            564 ACCTAGCTACAGAGTATCTTCAACTA 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      697 GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                 Disclosure; Fig 1; 55pp; English.
                                                                                                                                                                P-PSDB; AAU78285.
                                                                                                                                                                                                                                    (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA--- 639
                                                                                                                                                                                2002-304119/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour necrosis factor-related activation induced cytokine;
; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Tumour necrosis factor (ligand) superfamily,
member 11 (INFSF11), target region for antisense
nucleic acid. Specifically claimed in claim 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Human TRANCE (tumour necrosis factor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                    157..1110
                                                                                                                                                                                                             Marks SC;
                                                                                                                                                                                                                                                                                                                                                                               splice variant 1"
                                                                                                                                                                                                                                                                                                                                                                                            activation induced cytokine)
                                                                                                                                                                                                                                                                                                                                                                                              protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      443
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The present invention relates to a new method of treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth. The method of the invention involves administering

a tumour necrosis factor-related activation induced cytokine

CO

the mammal

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AAZ99964
ID AAZS
XX
AC AAZS
XX DNA
DE DNA
XX OSte
KW Coste
KW Inmm
XX Home
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5555555555555555555X
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                                                                        15-SEP-1998;
02-OCT-1998;
          (MEB<sub>I</sub>-) M &
                                                                                                                                                                           13-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                                                                                                                                         23-MAR-2000
                                                                                                                                                                                                                                                                                                          WO200015807-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding a human osteoprotegerin ligand (OPGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resulting from traumatic injury, surgery, osteoarthritis or rheumatoid arthritis, and disorders comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, carilaginea, exostosis bursata and multiple osteocartilaginous exostoses. The method is useful for inhibiting chondrocyte differentiation. The present nucleic acid sequence encodes the human TRANCE protein, splice variant 1, of the invention. TRANCE is a member of the tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ99964 standard; DNA; 2271 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TRANCE)-modulating agent. The method is useful for treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth, where the disorder comprising insufficient cartilage or skeletal growth is selected from dwarfism, osteopetrosis, craniofacial-skeletal discrepancies and bone or cartilage damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2226 BP; 656 A; 448 C; 505 G; 617 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      583 ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA--- 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  605 CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCTAGCTACAGAGTATCTTCAACTA 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCTAACTCTGCAGGACCTTCAGCTA 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---AAGGCATTTATTACCGGAATGCCGACAATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and acts directly on cartilage-producing cells (chondrocytes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.9%;
Similarity 72.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
      BIOTECH AS
                                                                    98DK-0001164.
98US-0102896.
                                                                                                                                                                    99WO-DK00481.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 185..1138
                                                                                                                                                                                                                                                                                                                                                          /product= "osteoprotegerin ligand"
                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteoporosis; bone resorption; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Pred. No. 8.3e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        æ
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                                                                                                                                                                                                                                                                                                                                                         RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                     Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
                                                                                                                                                                                          Human osteoprotegerin binding protein from the pcDNA/huOPGbpl.linsert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and amellorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                      Homo sapiens
                                                                                                            Paget's disease;
                                                                                                                   hypercalcaemia; osteoclast differentiation and activation receptor.
                                                                                                                                                                                                                                       11-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                AAV70285 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2271 BP; 658 A; 462 C; 522 G; 629 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a human osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein. The murine and human OPGL polypeptides are 87% homologous. O is a potent osteoclast differentiation factor when combined with CSF-
                                                                                                                                                                                                                                                                                                                                                                                                                                697 GCCTAACTCTGCAGGACCTTCAGCTA 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 75-77; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to treat, prevent and ameliorate osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halkier T, Haaning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                             ACCTAGCTACAGAGTATCTTCAACTA 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
             Location/Qualifiers 185..1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.9%; Score 126; DB 21; 72.6%; Pred. No. 8.4e-30;
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Best Local :
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16-APR-1997;
23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                          encoding OpG binding protein are used to produce recombinant OpG binding protein. OPG binding states are used in binding assays to determine osteoprotegrin (OG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful in immunoassays for detection of OpG binding protein) and to identify compounds that modulate binding of OpG binding protein to osteoclast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding OpG binding protein can be used to detect OpG binding protein-encoding sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for antisense regulation of OpG binding protein expression. Modulators of OpG binding protein, particularly soluble forms of OpG binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes human osteoprotegerin (OPG) binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 4; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boyle WJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9846751-A1
                                                                                                                                                                                                                                                                                                                                                  Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                          optionally in combination with agents that promote bone growth.
                                                                                                                                                                                                                                                                                                                                                                                     bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, loosening of prostheses,
                                                                                                                                                                                                                                                         465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                        525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
                                     873
                                                                                                                                        753
                                                                                                                                                                                                                                              CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1998-594578/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells transfected with vectors containing nucleic acid molecul
                                                            GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                           TTAATGCCACCGACATCCCCATCTGGTTCCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG
                                     ACCTAGCTACAGAGTATCTTCAACTA 898
                                                                                                   ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                                                        ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTAGCAATGGAAAACTAATAGTTAATC
                                                                                                                                                                 ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA---
                                                                                                                                                                                                                                                                                               193;
                                                                                      AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0052521.
97US-0842842.
97US-0880855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US07584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "osteoprotegerin binding protein"
                                                                                                                                                                                                                                                                                                         10.9%;
72.6%;
                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                           Score 126; DB 19, Pred. No. 8.4e-30
                                                                                                                                                                                                                                                                                                                       DB 19; Length 2274;
                                                                                                                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                               8;
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                 639
                                                                                                                                                                                           752
                                                                                      872
                                                                                                                                        812
                                                                                                                                                                                                                                                                                               2
                                                                        ABK40274
                         Matches
                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                       WPI;
465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
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08-MAR-1999
11-MAR-1999
11-MAY-1999
11-MAY-1999
22-JUN-1999
22-JUN-1999
22-JUN-1999
20-JUL-1999
26-JUL-1999
28-JUL-1999
28-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK40274 standard; cDNA; 2390 BP.
                                                                                                                                                        polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and anglogenic disorders. The polynucleotide sequences are also useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disoriflammatory disorder; immune disorder; angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding human PRO206 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-AUG-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; cytostatic; neuroprotective; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the isolation of novel human PRO
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 50; Fig 41; 302pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            malignancies, inflammatory, angiogenic and immunologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAU86148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                           Sequence 2390 BP; 778 A; 417 C; 506 G; 688 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marsters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-SEP-1999;
                                                                                                                                         polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-205567/26.
  193;
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SA,
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000WO-US03565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-US00219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan J, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-146222P.
99US-149395P.
99US-151689P.
99WO-US20111.
99WO-US21090.
99WO-US28313.
99WO-US28301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US28634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-144758P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-140650P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US12252
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99US-133459P
                      10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pitti RM, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Godowski PJ,
0
                      Score 126; DB 24; Pred. No. 8.6e-30;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gurney AL,
Smith V,
  65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         blastocoelic disorder;
                                           Length 2390;
Indels
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8
  Gaps
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RESULT 14
AAX80223
ID AAX80
XX AAX80
XX AAX80
AC AAAX80
XX TRANC
KW TRANC
KW TRANC
KW TNF-1
KW autoi
XX
HOMO
XX
FT CDS
FT CDS
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FT CDS
XX
FT CDS
XX
I1-DE
PR 11-DE
PR 11-DE
PR 12-DE
PR 11-DE
PR 12-DE
PR 12-DE
PR 11-DE
PR 12-DE
PR 11-DE
PR 12-DE
P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         뫄
cytckines (TRANCE). Human or murine TRANCE polypeptides or their variants, fragments, derivatives or analogues may be used as modulators of immune response in a mammal comprising, antisense sequences to TRANCE and fusion proteins comprising human and/or murine TRANCE. Agonists and antagonists of TRANCE, can be used to modulate immune response by increasing or decreasing the life span of mature dendritic cells and increasing or decreasing T cell activation. These techniques are especially useful for treating immune system related conditions such as HIV, cancer, autoimmune disease or hypersensitivity to an allergen. The TRANCE polypeptides can be used to increase the viability of dendritic cells in vivo or in vitro, especially when used in conjunction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-DEC-1998;
12-DEC-1997;
03-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 1; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNF like proteins for treating autoimmunity and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANCE; tumour necrosis factor superfamily; signal transduction; TNF; TNF-related activation induced cytokine; immune response; cancer; autoimmune disease; HIV; hypersensitivity; allergen; ds.
                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes human TNF~related activation induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human TRANCE encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9929865-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999-385609/32.
DB; AAY17873.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Josien R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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97US-0989479.
98US-0034099.
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1..738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steinman R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1823 BP
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Best Local
The present sequence is the coding sequence for Differentiation Factor (ODF). ODF is thought to
                                      Claim 1;
                                                                    Novel nucleic acid encoding rat osteoclast differentiation factor useful for modulating activity of a cell, e.g., cell proliferation
                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                             P-PSDB; AAB82092
                                                                                                                                                Xu J,
                                                                                                                                                                      (UYWA-) UNIV WESTERN AUSTRALIA.
                                                                                                                                                                                               29-SEP-1999;
                                                                                                                                                                                                                      29-SEP-2000;
                                                                                                                                                                                                                                             05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                     Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                            Osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                           Rat osteoclast differentiation factor, ODF, coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF86481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF86481 standard; cDNA; 957
                                                                                                                                                                                                                                                                    WO200123549-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1823 BP; 569 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD40L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                              differentiation
                                                                                                                                                                                                                                                                                                                                                                                         osteoclast
                                                                                                                        2001-335526/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTGCTAGGAAACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCTAGCTACAGAGTATCTTCAACTA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCGGGGGTGGGGTAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGGAAAACTAAGAGTCA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or TNF-alpha).
                                                                                                                                               Zheng
                                      Fig 1; 81pp;
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                                                                                                                                                                                                                                                                                                                                                                        clast formation inducer; vaccine; gene therapy;
Differentiation Factor; bone; ss.
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                                                                                                                                                                                             99AU-0003147.
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 1..957
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                                                            and cell viability
                                      English.
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Pred. No. 8.1e
0; Mismatches
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rat Osteoclast
be directly in
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                                                                      proliferation,
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Search completed: December 8, 2002, 17:26:08 
 Job time : 341.592 \ \text{secs}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the differentiation of monocytes/macrophages into osteoclasts. Osteoclasts promote dissolution of the bone matrix and solubilisation of bone salts. The present sequence is useful in gene therapy, and as hybridisation probes or primers. ODF protein is useful for modulating the activity of cells, e.g., cell proliferation, cell differentiation and cell viability, as immunogens to generate anti-rat ODF antibodies, and as vaccines. Anti-rat ODF antibodies are useful in assay methods for quantifying ODF polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 957 BP; 230 A; 260 C; 256 G; 211 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                             595 AACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC 654
                                                                                                                                                                                                                                                                                 606 AACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAAT 659
                                                                                                                                                                                                                                                                                                                                                 535
                                                                                                                                                                                                                                                                                                                                                                 548 GG--CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 605
                                                                                                                                                                                              660 GCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAG 719
                                                                                                                              720 CT 721
                                                                                                                                                                        655 GCCAACATTTGCTTCAGGCATCATGAAACCTCAGGGAGCGTACCTGCGGACTATCTTCAG 714
                                                                                                                                                                                                                                                                                                                                        GGTTCCCATAAAGTCAGTCTGTCCTCTTGGTACCATGATCGAGGCTGGGCCCAAGATCTCT 594
                                                                                      CT 716
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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
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 GenEmbl:*

1: gb_ba:*

2: gb_ht;

3: gb_ln:*

4: gb_om:*

6: gb_ph:

6: gb_ph:

8: gb_ph:

9: gb_r(

11: gb_s'

12: gb_s'

13: gb_u

14: gb_u

15: em_l

16: em_l

17: em_l

18: em_l

21: em_l

22: em_l

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41:
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13590.225 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 aaaagaggataattcaagaa.....taataaaaggaggaaaatgc 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-880-457-1
1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maximum Match 100%
Listing first 45 summaries
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gb_pat:*
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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1 AC104794 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		Result No. 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
	97 97 97 94.4 94.8 81.6 81.6 81.6 81.6 81.6	126 126 126 126 126 122 122 97 97 97 97 97 97 97	Score 467.4 467.4 268 208 126 126 126 126
AC104794 Homo sapiens 3 unordered AC104794 AC104794.3 HTG: HTGS_PH HOMO sapiens Eukaryota; M Mammalia; Eu 1 (bases 1 1 the sequence	4444 20000314444 20000314444	110.99 110.99 110.99 110.99 110.99	000000744000164
165707 bp DNA chromoscme 2 clone RP11-254 pieces. 31:20340520 ASE1; HTGS_DRAFT; HTGS_ACTIV etazoa; Chordata; Craniata; theria; Primates; Catarrhini to 165707) H. of Homo sapiens clone	11 2 1	954 972 1034 22201 2297 2390 1823 113451 200724 951 951 951 951 1630 1630 1630	Length 165707 190748 1186 117250 157250 157250 911 911 930 954
		00000000000000000000000000000000000000	
	AF019048 AF01918 AF012119 AR062119 AF053713 AX232589 AC094149 E34349 AB022036S4 AC126690 166494 AC012454 AC012454 AC083795	AX451895 AB064269 AB064269 AF019047 AF057712 AF053712 AF013171 AF187319 AC022297 AL139382 AB032771 AB032771 AB032771 B34350 E36388 AB06426 AB0036798 AR156433 AR16417 AX147887 AX167889 AR157658	ID AC104794 AC010969 AX358828 AX358221 AC027264 AB064268 AB064268 AB06427 AB037599 AB037599 AR156434
linear HTG 30-APR-2002 F7, WORKING DRAFT SEQUENCE, EFIN. Vertebrata; Euteleostomi; Hominidae; Homo.	AF019048 Mus muscu AF013170 Mus muscu AF062119 Sequence AF053713 Mus muscu AX232589 Sequence AC094149 Rattus no E34349 DNA and pro AB022039 Mus muscu AC126690 Mus muscu AC126494 Sequence 14 AC012454 Homo sapi AC083795 Homo sapi	AX451895 Sequence AB064270 Homo sapi AB064270 Homo sapi AB064269 Homo sapi AF019047 Homo sapi AF019171 Homo sapi AX201362 Sequence AF013171 Homo sapi AF187319 Rattus no AC023297 Homo sapi AL139382 Human DNA AB032772 Mus muscu AB032771 Mus muscu AB032771 Mus muscu E34350 DNA and pro E36388 Novel prote AB008426 Mus muscu AB036798 Mus muscu AB036798 Mus muscu AB036798 Mus muscu AR156433 Sequence AX147987 Sequence AX147987 Sequence AX1471652 Sequence AX1671652 Sequence	Description AC1104794 Homo sapi AC010969 Homo sapi AC0358828 Sequence AX358213 Sequence AC027264 Homo sapi AB064268 Homo sapi AB061227 Homo sapi AB037599 Homo sapi AB037599 Homo sapi AB156434 Sequence AR164148 Sequence AR164148 Sequence AX147989 Sequence

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                                                                                                                 Matches 468;
                                                                                                                                                             Query Match
40150 AAAAGAGGATAATTCAAGAAGGGCTTCTTTAAGGGACTATTTCCCAAGATGGGAATGGAG 40209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                        Local
                            1 AAAAGAGGATAATTCAAGAAGGGCTTCTTTAAGGGACTATTTCCCAAGATGGGAATGGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: MI3; 08
Sequencing vector: plasmid; 108
Chemistry: Dye-primer ET; 08 of reads
Chemistry: Dye-terminator Big Dye; 1008 of reads
Chemistry: Dye-terminator Big Dye; 1008 of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 162662 bases at least 040
Consensus quality: 163189 bases at least 030
Consensus quality: 164786 bases at least 020
Insert size: 9479; agarose-fp
Insert size: 167795; sum-of-contigs
Quality coverage: 12.78 in 020 bases; sum-of-contigs
Quality coverage: 10.53 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                        /note="assembly_name:Contig68"
76328. .165707
/note="assembly_name:Contig69"
42887 a 42242 c 39083 g 41295 t
                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (30-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Apr 30, 2002 this sequence version replaced gi:19339129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
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Submitted (21-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: H_NH0254F07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as soon as it is available and the accession number will
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                 /note="assembly_name:Contig21"
1213. .76227
                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP11-254F7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .165707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1112: contig of 1112 bp in length
1212: gap of unknown length
76227: contig of 75015 bp in length
76327: gap of unknown length
165707: contig of 89380 bp in length
                                                                                                                                   40.3%;
99.8%;
                                                                                               Score 467.4; DB 2; Length 165707;
Pred. No. 5.3e-134;
0; Mismatches 1; Indels 0;
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REFERENCE
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SOURCE
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Submitted (07-NOV-2001) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis,
                                                                                                         Submitted (20-APR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                        Direct Submission
                                                                                                                                                   Waterston, R.H.
Direct Submission
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Submitted (19-APR-2001) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (28-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                               Waterston, R.
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1 (bases 1 to 190748)
Sulston, J. E. and Waterston, R.
Toward a Complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
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Homo sapiens BAC clone RP11-95D17 from 2, complete sequence.
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Missouri 63108,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on Apr 19, 2001 this sequence version replaced gi:11128441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The clone sequenced to the left is Rp11-521D12. Actual staths clone is at base position 1 of Rp11-95D17; actual end base position 190748 of Rp11-95D17.
                                                                                                                                                                                                                                                                                                                                                                                                          Unresolved tandem repeat from base position 181200 to 187300. Sinformation from restriction digest suggests that the full repeat may not be represented.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: H_NH0095D17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center Center code: WUGSC
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                                                         /rpt_family="MIR" 2626. .3646
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806. .1114
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                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                /rpt_family="MIR"
2179. .2369
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325. .805
                                                                                                                                                                                                                                                                                           /clone="RP11-95D17"
                                                                                                                                                                                                                                                                                                                                  /chromosome="2"
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/rpt_family="AT_rich"
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8242. .8532
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              /note="similar to 13729, .14126 /note="similar to 13735, .13801
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10647. .10948
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12335. .12416
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13630. .14128
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13557. .13667
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12955. .13065
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12698. .12954
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12467. .12594
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                                                                                                                         Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watanabe,C.K. and Wood,W.I.
                                                                 Genentech Inc. (US)
                                                                                                     Secreted and transmembrane polypeptides and nucleic acids encoding
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                           Sequence 81 from Patent WO0193983. 
AX358828
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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14422. .14474
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Local Similarity 100.0%; Pred. No. 5.9e-72;
hes 268; Conservative 0; Mismatches 0; Indels (
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Secreted and transmembrane polypeptides and nucleic acids encoding
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Homo sapiens chromosome 2 clone RP11-164P8 map 2, WORKING DRAFT
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Mammalia; Eutheria;
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Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L.,
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Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141 USA On Oct 4, 2000 this sequence version replaced gi:7331634. All repeats were identified using page 2017.
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FEATURES
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 155000; agarose-fp
Insert size: 155250; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 4.1 in Q20 bases; sum-of-contigs
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82120 107411
107412 107511:
107512 116168
                                                             107412 107511: gap of 100 bp
107512 116168: contig of 8657 bp
116169 116268: gap of 100 bp
116269 128458: contig of 12190 b
128459 128558: gap of 100 bp
128459 1467712: contig of 18154 b
                        146713 146812: gap of 100 bp
146813 157250: contig of 10438 bp in length
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12726 15710: contig of 2985 bp in length
15711 15810: gap of 100 bp
15811 19721: contig of 3911 bp in length
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12626 12725: gap of
12726 15710: cont
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71872 71971: gap of
71972 82019: cont
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64505 71871: contig of 7367 bp in length
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47417 47516:
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32776 4040
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6238 8049: contig of 1812 bp in length
8050 8149: gap of 100 bp
8150 12625: contig of 4476 bp in length
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Location/Qualifiers
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40400: contig of 7625 bp
0500: gap of 00 bp
47416: contig of 6916 bp
7516: gap of 100 bp
7516: gap of 100 bp
66473: contig of 9227 bp
                                                                                                                                                                                                    1119: gap of 100 bp 107411: contig of 25292 bp in length
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24311: contig of 4490 k
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                                                                                                                                                                                                                                                     971: gap of 100 bp
82019: contig of 10048 bp in length
                                                                                                                                                                                                                                                                                                                                             343: gap of 100 bp
64404: contig of 7561 bp in length
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6137: contig of 2088 bp in length
7: gap of 100 bp
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0: gap of 100 bp
2288: contig of 1288 bp in length
                                                                    contig of 18154 bp in length
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                                                                                                 149185 GCAATGTCCTTGAGAAGACCCTGTCTTAATCATCTCTGTGTCTCACGCCTGGCTCATAAC 149126
1122 ATATGCTTATCGCATGCTTTTAATAAAAGGAGGAAAATGC 1161
                                                           1062 GCAATGTCCTTGAGAAGACCCTGTCTTAATCATCTCTGTGTGTCTCACGCCTGGCTCATAAC 1121
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47517. .56743
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146813. .157250
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128559. .146712
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116269. .128458
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32776. .40400
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24412. .32675
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/note="assembly_fragment"
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/db_xref="taxon:9606"
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95.5%;
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Pred. No. 9.8e-52;
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AUTHORS
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VERSION
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AB064268
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Best Local Similarity
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                                                                    493 AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
553 ACCTAGCTACAGAGTATCTTCAACTA 578
                                                                                                         640 ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
                                                                                                                                             433 ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC 492
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                                                                                                                                                                                                                        373 TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG
                                                                                                                                                                                                                                                 525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
                                                                                                                                                                                                                                                                                                     313 CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 372
                                                                                                                                                                                                                                                                                                                                        465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                    GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ikeda, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ikeda,T., Kuroyama,H. and Hirokawa,K.
Determination of human RANKL isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax:81-3-5803-0123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDI
PSGSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLAT
EYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAB79693.1"
/db_xref="GI:18143617"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="receptor activator of nuclear factor kappa
ligand 3"
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Pred. No. 1.3e-27;
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ORGANISM

Homo sapiens

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                                                                                                                                                                                                                           GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                           ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                                                                                                                                                                                                                                                             ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC 585
                                                                                                                                                                                                                                                                                                                                                                                                                   TTAATGCCACCGACATCCCATCTGGTTCCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG
Homo sapiens male tongue epithelial-like squamous cell_line:SCC-4 cDNA to mRNA.
                                                                          Homo sapiens mRNA for sODF/TRANCE, AB037599
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Homo sapiens mRNA for hRANKL
AB061227
                                                         AB037599.1 GI:6863047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-MAY-2001) Tohru Ikeda, Graduate School, Tokyo Medical and Dental University, Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
                                                                                                                AB037599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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/db_xref="G1:16610213"
/db_xref="G1:16610213"
/db_xref="G1:16610213"
/translation="MEVALLGLEGQVVCSVALFFYFRAQMDPNRISEDGTHGTYRIL
RLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDG
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VNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWS
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                                                                                                                                                                                                                      GCCTAACTCTGCAGGACCTTCAGCTA 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193;
                                      Sequence 12 from patent US 6242213. AR156434
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Location/Qualifiers
                 AR156434.1
                                                                             AR156434
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Cancer cells responsible for humoral hypercalcemia express mRNA encoding a secreted form of ODF/TRANCE that induces osteoclast
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/protein_id="baa90488.1"
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PSGSHKVSLSSWYDDFGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLAT
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EVSNPSLLDPDQDATYFGAFKVRDID"
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/tissue_type="tongue"
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/db_xref="taxon:9606"
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509 TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCCTCTGGTACCATG 568
                                                                             525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCGGAAACATG 582
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Dougall,W.C. and Galibert,L.
Receptor activator of NF-, kappa.B
Patent: US 6271349-A 12 07-AUG-2001;
Location/Qualifiers
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0; Mismatches 65;
                                                                                                                                                         Score 126; DB 6; Length 954; Pred. No. 1.3e-27; O; Mismatches 65; Indels
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AX451895 954 bp
Sequence 5 from Patent WO0224896.
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/protein_id="CAC41185.1"
/db_xref="GI:14346965"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                           AB064270 972 bp mRNA linear PRI 26-DEC-
HOMO sapiens hRANKL 2-2 mRNA for receptor activator of nuclear
factor kappa B ligand 2-2, complete cds.
                              Determination of human RANKL isoforms
                                                                                                                           Homo sapiens
                                                Ikeda,T., Kuroyama,H. and Hirokawa,K.
                                                                                                                                             Homo sapiens cDNA to mRNA.
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SRSMFVALLGLGLGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDT
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EAQPFAHLTINAFDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYA
NICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSIN
VGGFFKLKSGEEISIEVSNPSLLDPPQDATYFGAFKVRDID"
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/db_xref="taxon:9606"
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Ikeda,T. and Kuroyama,H.
Direct Submission
Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                              Unpublished
                                                                                                                Determination of human RANKL isoforms
                                                                                                                                    Ikeda,T., Kuroyama,H. and Hirokawa,K.
                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                         Homo sapiens cDNA to mRNA.
                                                                                                                                                                                                                                                                                     AB064269.1 GI:18143618
                                                                                                                                                                                                                                                                                                                           Homo sapiens hRANKL 1 mRNA for kappa B ligand 1, complete cds.
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VNQDGFYYLYANICFRHHETSGDLAFEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWS
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1 219 c 249 g 234 t
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/db_xref="taxon:9606"
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72.6%;
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                                                   JOURNAL MEDLINE
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Best Local Similarity
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                                                                                                                                                                                                                                                       ORGANISM
                                                                                                               TITLE
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                                     PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCTAGCTACAGAGTATCTTCAACTA 794
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                                                                                                                                                                                                                                                                                                                                       2201 bp mRNA linear PRI 22-NOV-19 (RANKL) mRNA, complete cds.
                                                                    growth and dendritic-cell function
Nature 390 (6656), 175-179 (1997)
                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2201)
                                                                                                                                            Anderson, D.M., Maraskovsky, E., Billing Tometsko, M.E., Roux, E.R., Teepe, M.C.,
                                     9367155
                                                       98032977
                                                                                                               A homologue of the TNF receptor and its ligand enhance T-cell
                                                                                                                                                                                                                                                                         Homo sapiens.
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(bases 1 to 2201)
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81. .1034
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257 c 265 g 237 t
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                                                                                                                                                                      Maraskovsky, E., Billingsley, W.L.,
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Pred. No. 1.3e-27;
0; Mismatches 65
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                                                                                                                                                        DuBose, R.F.,
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                                                                                                                                                      Cosman, D. and
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                                                                         817 ACCTAGCTACAGAGTATCTTCAACTA 842
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                                                                                                            GCCTAACTCTGCAGGACCTTCAGCTA 722
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Submitted (13-AUG-1997) Molecular Biology,
University St., Seattle, WA 98101, USA
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igand"
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Pred. No. 1.4e-27;
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